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OM protein - protein search, using sw model

Run on: September 21, 2001, 16:51:56 ; Search time 22.23 Seconds  
(without alignments)  
1475.375 Million cell updates/sec

Title: US-09-236-468A-2  
Perfect score: 2907  
Sequence: 1 MAMLGASLHVWGLMLGSL.....DDILMEKSPRMESNPDTG 541

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues  
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
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7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
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9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
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14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	2907	100.0	541	18	AAW12695
2	2635	90.6	550	22	AAW71875
3	2626	90.3	550	22	AAW80560
4	2217.5	76.3	546	22	AAW80559
5	1418.5	48.8	536	21	AAW99600
6	1418.5	48.8	536	21	AAW90230
7	1392	47.9	585	17	AAW92276
8	1392	47.9	585	20	AAW73315
9	1391	47.9	585	13	AAW27705
10	1388	47.7	515	17	AAW92275
11	1388	47.7	515	20	AAW73314

12	1375	47.3	515	13	AAW27704
13	1336.5	46.0	593	22	AAW71876
14	1331.5	45.8	591	17	AAW92277
15	1331.5	45.8	591	20	AAW73316
16	1331.5	45.8	593	20	AAW73317
17	1323.5	45.5	591	13	AAW27706
18	1313	45.2	593	17	AAW92278
19	1307.5	45.0	542	21	AAW99601
20	1303.5	44.8	614	13	AAW27707
21	1302.5	44.8	523	21	AAW90231
22	1043	35.9	448	21	AAW96986
23	1043	35.9	450	21	AAW96988
24	1041	35.8	435	21	AAW96987
25	1038	35.7	446	21	AAW96983
26	1036	35.6	435	21	AAW07529
27	1007.5	34.7	335	21	AAW96984
28	1005.5	34.6	324	21	AAW96985
29	801	27.6	449	13	AAW30187
30	785	27.0	458	16	AAW72506
31	784	27.0	440	22	AAW71877
32	776	26.7	440	21	AAW08188
33	772.5	26.6	459	14	AAW42848
34	759.5	26.1	457	22	AAW71878
35	731	25.1	419	22	AAW19981
36	713.5	24.5	437	19	AAW80309
37	713.5	24.5	437	20	AAW92973
38	708	24.4	437	16	AAW70136
39	704	24.2	431	19	AAW80310
40	704	24.2	431	20	AAW92974
41	702.5	24.2	438	19	AAW80308
42	702.5	24.2	438	20	AAW92972
43	702	24.1	438	22	AAW71879
44	696.5	24.0	448	15	AAW58666
45	696.5	24.0	467	15	AAW58656

## ALIGNMENTS

RESULT 1  
AAW12695  
ID AAW12695 standard; Protein; 541 AA.  
XX  
AC AAW12695;  
XX  
XX  
DT 31-MAY-1997 (first entry)  
XX  
DE G-protein parathyroid hormone receptor HLTG74.

XX G-protein parathyroid hormone receptor; HLTG74; parathormone; PTH;  
KW calcium; signal transduction; agonist; antagonist; hypocalcaemia;  
KW hyperphosphataemia; hypoparathyroidism; chronic tetany;  
KW osteoporosis; hypercalcaemia; hypoparathyroidism; hypophosphataemia;  
KW kidney stone; nephrolithiasis; therapy; diagnosis.  
OS Homo sapiens.  
XX  
XX WO639433-A1.  
PN  
PD 12-DEC-1996.  
XX  
XX 05-JUN-1995; 95WO-US07085.  
XX  
XX 05-JUN-1995; 95WO-US07085.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Li Y, Rosen CA, Ruben SM, Soppet DR;  
XX WPI; 1997-043068/04.  
XX N-PSDB; AAW59619.  
XX  
XX Human G-protein parathyroid hormone receptor, HLTG74 - used to

Opossum kidney PTH  
Human PTRR seven t  
Rat bone PTH/pTHR  
Parathyroid hormon  
Human Parathyroid  
Rat bone PTH/pTHR  
Human kidney PTH/p  
zebrafish parathyro  
Human kidney PTH/p  
zebrafish PTH3R re  
Human tethered PTH  
Human tethered PTH  
Human tethered PTH  
Tethered PTH-1 rec  
A mutant parathyro  
Tethered PTH-1 rec  
Tethered PTH-1 rec  
Secretin receptor.  
Porcine vasoactive  
Human SCRC seven t  
Amino acid sequenc  
VIP receptor prote  
Human VIPR seven t  
Chicken growth hor  
Rat PACAP/VIP R-2  
Rat PACAP/VIP R-2  
Rat vasoactive int  
Human PACAP/VIP R-  
Human PACAP/VIP R2  
Human PACAP/VIP R-  
Human PACAP/VIP R-  
Human VIPs seven t  
Rat PACAP receptor  
Rat PACAP receptor

PT identify (ant)agonists, used in the treatment of hypo- or  
PT hyper-calcaemia, hypo- or hyper-phosphatemia, kidney stones, etc  
XX  
PS Claim 9; Fig 1A-E; 62pp; English.  
XX  
XX A novel 7-transmembrane receptor (AAW12695) has been identified as a  
CC human G-protein parathyroid hormone (PTH) receptor, designated  
CC HLTDG74. It shows 48.2% homology to the human PTH receptor. Its  
CC amino acid sequence was deduced from a cDNA clone (AAW59619) isolated  
CC from a human T cell lymphoma tissue cDNA library. Recombinant  
CC HLTDG74 can be produced in transformed host cells and used to  
CC screen for (ant)agonist cpds. Agonists may be used to prevent or  
CC treat e.g. hypocalcaemia, hyperphosphataemia, hypoparathyroidism  
CC and chronic tetany by stimulating an increase in serum calcium  
CC levels. Antagonists can be used to inhibit the receptor e.g. for  
CC the treatment of osteoporosis, hypercalcaemia, hypoparathyroidism,  
CC hypophosphataemia, kidney stone, nephrolithiasis.  
XX  
SQ Sequence 541 AA;

Query Match 100.0%; Score 2907; DB 18; Length 541;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLSLHWGMLGSCLLARALDSQGTITIEQIVLVKAKVQCELNITIAQLQEGE 60  
DB 1 mawlgaslhvwmglgscllaraqlsdsgtittieqivlvkavqcelnitaqlqege 60  
QY 61 GNCFPEDWGLICWPRGTGKISAVPCPPYIYDFNHNKGVAFRHCNPNGTWDFMHSLNKTTWA 120  
DB 61 gncfpewdglicwprgtvgkisavpcppyiydfnhkgvafrcnpgntwdfmhslnktwa 120  
QY 121 NYSDDLRFLOPDISIGKQECERLYVMYTVGYSISFSGSLAVAILIIGYFRRLHCTRNYYIH 180  
DB 121 nysdclrflopdgisigkqecerylvmtyvgyisfsgslavailiigyfrlrhctrnyih 180  
QY 181 MHLFVSFMLRATSFIVKDRVVAHIGVKELESIMODDPONSIEATSVDKSQYIGCKIAV 240  
DB 181 mhlvsvfmlratsifvkdrrvvahigvkeleslimoddpnseatsvdksgyigckia 240  
QY 241 VMTIYFLATNYWILVEGLYHNLIFVAFSDTKYLWGFILIGWGPAAFPAAVAAVARAT 300  
DB 241 vmtiyflatnywvllveglyhnlifvafsdtkylwgflligwgpaaftvaavavarat 300  
QY 301 LADARCELSAGDIKWTYQAPIIAAGLNFIPLNTVRLVATKIWETNAVGHDTKQYRK 360  
DB 301 ladarcelsagdikwtYQAPIIAAGLNFIPLNTVRLVATKIWETNAVGHDTKQYRK 360  
QY 361 LAKSTLVLVLFVGVHYIVFVCLPHSTGLGWEIRHCELFNFNSFGFFVSIICYCNGEV 420  
DB 361 lakstlvlvlfvghyivfvclphstglgweirmhcelffnfsfgffvsiilcycng 420  
QY 421 QAEVKKWSRWNLSDWKRTPPCGSRRCGSVLTVTYHSTSSQVAAAHAWCLSLAKLPR 480  
DB 421 qaevkkwswrwnlsdwrtpcpgrcsrvtvtvtyhstssqvaaahawclslaklpr 480  
QY 481 SPADSLTATSLYLAMSGVTSQTSRHTSLSPRSNKEDSGRQDDILMEKSPRMESNPDT 540  
DB 481 spadslatatslylamsgvtsqtsrhtslsprsnkedsgrqddilmeksprmesnpdte 540  
QY 541 G 541  
DB 541 g 541

RESULT 2  
AAB71875  
ID AAB71875 standard; Protein; 550 AA.  
AC AAB71875;  
XX  
DT 03-MAY-2001 (first entry)

XX  
DE Human PTR2 seven transmembrane domain.  
XX  
KW Human; PTR2; parathyroid hormone receptor; hl5571; immunomodulatory;  
KW vascular; hepatic; antiasthma; antimicrobial; antiinflammatory;  
KW immunosuppressive; gene therapy; vaccine; G-protein coupled receptor;  
KW GPCR; liver fibrosis; respiratory disorder; infection;  
KW chronic inflammatory disease; organ-specific autoimmunity;  
KW graft rejection; cystic fibrosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200109328-A1.  
XX  
PD 08-FEB-2001.  
XX  
PF 03-AUG-2000; 2000WO-US21278.  
XX  
PR 03-AUG-1999; 99US-0146916.  
PR 29-FEB-2000; 2000US-0515781.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Hodge MR, Lloyd C, Weich NS;  
XX  
XX WPI; 2001-138653/14.  
XX  
XX Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful  
PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma  
PT -  
XX  
XX Disclosure; Fig 2; 145pp; English.  
XX  
CC The present sequence is a human G-protein coupled receptor (GPCR) used  
CC for comparison with the seven transmembrane domain of a novel GPCR  
CC designated hl5571. hl5571 GPCR polynucleotides and polypeptides may be  
CC used in the prevention, treatment and diagnosis of diseases associated  
CC with inappropriate GPCR expression. Such diseases includes immune,  
CC haematological, fibrotic, hepatic and respiratory disorders including  
CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic  
CC infections, chronic inflammatory diseases, organ-specific autoimmunity,  
CC graft rejection, graft versus host disease, cystic fibrosis and, in  
CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens  
CC in the production of antibodies against GPCR and in assays to identify  
CC modulators (agonists and antagonists) of GPCR expression and activity.  
CC The anti-GPCR antibodies and GPCR antagonists may also be used to down  
CC regulate GPCR expression and activity. The anti-GPCR antibodies may be  
CC used as diagnostic agents for detecting the presence of GPCR  
CC polypeptides in samples.  
XX  
SQ Sequence 550 AA;

Query Match 90.6%; Score 2635; DB 22; Length 550;  
Best Local Similarity 91.4%; Pred. No. 2.3e-277;  
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;

QY 1 MAWLGLSLHWGMLGSCLLARALDSQGTITIEQIVLVKAKVQCELNITIAQLQEGE 60  
DB 1 mawlgaslhvwmglgscllaraqlsdsgtittieqivlvkavqcelnitaqlqege 60  
QY 61 GNCFPEDWGLICWPRGTGKISAVPCPPYIYDFNHNKGVAFRHCNPNGTWDFMHSLNKTTWA 120  
DB 61 gncfpewdglicwprgtvgkisavpcppyiydfnhkgvafrcnpgntwdfmhslnktwa 120  
QY 121 NYSDDLRFLOPDISIGKQECERLYVMYTVGYSISFSGSLAVAILIIGYFRRLHCTRNYYIH 180  
DB 121 nysdclrflopdgisigkqecerylvmtyvgyisfsgslavailiigyfrlrhctrnyih 180  
QY 181 MHLFVSFMLRATSFIVKDRVVAHIGVKELESIMODDPONSIEATSVDKSQYIGCKIAV 240  
DB 181 mhlvsvfmlratsifvkdrrvvahigvkeleslimoddpnseatsvdksgyigckia 240

Qy 241 VMFYFLATNYWIIWEGLYLHNLIFVAFSDTKYLMGFFILIGWGFPAAFVAANAVARAT 300  
 Db 241 VMFYFLATNYWIIWEGLYLHNLIFVAFSDTKYLMGFFILIGWGFPAAFVAANAVARAT 300  
 Qy 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDRKQYRK 360  
 Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDRKQYRK 360  
 Qy 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGFVSIYCYCNGEV 420  
 Db 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGFVSIYCYCNGEV 420  
 Qy 421 QAEVKMWSRWNLSDVKMRTPCGSRRCGSLVTTVTHSTSSQSOVAAAHAMCL---SLAK 477  
 Db 421 QAEVKMWSRWNLSDVKMRTPCGSRRCGSLVTTVTHSTSSQSOVAAAHAMCL---SLAK 477  
 Qy 478 LPRSPADSLTATSLYLAWSGVYQTSRTASHTLS---TRSNKEDSGRQRDDILMEKPSRPM 534  
 Db 481 IASRQPS-----hitlpgyvwnsnseqdciphsfheetkedsgrgddilmekpsr 534  
 Qy 535 SNPDTEG 541  
 Db 535 snpdteg 541

RESULT 3  
 AAB80560  
 ID AAB80560 standard; Protein: 550 AA.  
 AC AAB80560;  
 DT 26-APR-2001 (first entry)  
 DE Human PTH2 receptor amino acid sequence.  
 KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;  
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; leptonic;  
 KW PTH2 receptor binding activity; antidiabetic; osteoporosis; neuroleptic; analgesic;  
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiac;  
 KW cytosolic; antiasthmatic; neuroprotective; PTH receptor antagonist;  
 KW obesity; eating disorder; metabolic disorder; mental disorder;  
 KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;  
 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;  
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;  
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;  
 KW leukodystrophy.  
 XX Homo sapiens.  
 XX WO200077042-A2.  
 XX 21-DEC-2000.  
 XX 15-JUN-2000; 2000WO-US16776.  
 XX 15-JUN-1999; 99US-0139335.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Usdin TB, Hoare SRJ;  
 XX WPI; 2001-122833/13.  
 PT New parathyroid hormone type 2 or 1 receptor ligand, useful for  
 PT treating e.g. migraine or headaches, hypertension, obesity and other  
 PT eating or metabolic disorders, mental disorders and osteoporosis -  
 XX Example 4; Fig 1; 106pp; English.  
 CC The present invention describes an isolated or purified peptide (I) that  
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1  
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidiabetic,  
 CC neotropic, analgesic, antimigraine, antidiabetic, osteopathic,

CC hypertensive, cardiac, cytostatic, antiasthmatic and neuroprotective  
 CC activities, and is an PTH receptor antagonist. The peptide is useful in  
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.  
 CC The PTH2 receptor binding activity may be used in treating obesity or  
 CC other eating or metabolic disorders, mental disorders (e.g. depression,  
 CC schizophrenia and dementia), acute or chronic pain, migraine or  
 CC hypercalcaemia and other disorders affecting calcium metabolism,  
 CC hypertension, congestive heart failure and control of tumour growth,  
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating  
 CC conditions such as multiple sclerosis and leukodystrophies. The present  
 CC sequence represents a PTH2 receptor which is used in the  
 CC exemplification of the present invention.  
 XX  
 XX Sequence 550 AA;  
 Qy Query Match 90.3%; Score 2626; DB 22; Length 550;  
 Best Local Similarity 91.2%; Pred. No. 2.2e-276;  
 Matches 499; Conservative 6; Mismatches 30; Indels 12; Gaps 3;  
 Qy 1 MAWLGLSLHVMGLMGLSCLLARAQLDSGRTITIEQIVLVLKAKVOCLELNTAOLGE 60  
 Db 1 maglglslhvmglmglsccllaraqldsgdtitieeqivlvkavqcelnitaqlge 60  
 Qy 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIYDFNHNKGVAFRCNPNGTWDFMHSLNKTWA 120  
 Db 61 gncfpewdglcwpgrgtvgkisavpcppyiydfnhkgyafrcnpgtwdfmhslnktwa 120  
 Qy 121 NYSCLRFQLPDISIGKOEFCERLYVMYTVGYSISFGSLAVAILIIGYPRRLHCTRNTH 180  
 Db 121 nysclrfqlpdisigkqefferyvmtyvgysisfgslavailiigyfrlthctrnyih 180  
 Qy 181 MHLFVSFMLRATSIKDRVVAHAGVKELESIMQDDPQNSIEATSDKSOYIGCKIAV 240  
 Db 181 mhlfvsfmlratsikdrvvahagvkelesimqddpqnseatsvdksgyigcklav 240  
 Qy 241 VMFYFLATNYWIIWEGLYLHNLIFVAFSDTKYLMGFFILIGWGFPAAFVAANAVARAT 300  
 Db 241 VMFYFLATNYWIIWEGLYLHNLIFVAFSDTKYLMGFFILIGWGFPAAFVAANAVARAT 300  
 Qy 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDRKQYRK 360  
 Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDRKQYRK 360  
 Qy 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGFVSIYCYCNGEV 420  
 Db 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGFVSIYCYCNGEV 420  
 Qy 421 QAEVKMWSRWNLSDVKMRTPCGSRRCGSLVTTVTHSTSSQSOVAAAHAMCL---SLAK 477  
 Db 421 QAEVKMWSRWNLSDVKMRTPCGSRRCGSLVTTVTHSTSSQSOVAAAHAMCL---SLAK 477  
 Qy 478 LPRSPADSLTATSLYLAWSGVYQTSRTASHTLS---TRSNKEDSGRQRDDILMEKPSRPM 534  
 Db 481 IASRQPS-----hitlpgyvwnsnseqdciphsfheetkedsgrgddilmekpsr 534  
 Qy 535 SNPDTEG 541  
 Db 535 snpdteg 541

RESULT 4  
 AAB80559  
 ID AAB80559 standard; Protein: 546 AA.  
 AC AAB80559;  
 DT 26-APR-2001 (first entry)  
 DE Rat PTH2 receptor amino acid sequence.  
 XX Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;

parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic; PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic; antimigraine; antidiabetic; osteopathic; hypertensive; cardiant; cytotatic; antisthmatic; neuroprotective; PTH receptor antagonist; obesity; eating disorder; metabolic disorder; mental disorder; depression; schizophrenia; dementia; acute pain; chronic pain; migraine; headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism; hypertension; congestive heart failure; tumour; asthma; emphysema; restrictive lung disease; demyelinating condition; multiple sclerosis; leukodystrophy.

Rattus sp.

WO200077042-A2.

21-DEC-2000.

15-JUN-2000; 2000WO-US16776.

15-JUN-1999; 99US-0139335.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Usdin TB, Hoare SRJ;

WPI: 2001-122833/13.

New parathyroid hormone type 2 or 1 receptor ligand, useful for treating e.g. migraine or headaches, hypertension, obesity and other eating or metabolic disorders, mental disorders and osteoporosis -

Example 4; Fig I; 106pp; English.

The present invention describes an isolated or purified peptide (I) that is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1 receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression, nootropic, analgesic, antimigraine, antidiabetic, osteopathic, hypertensive, cardiant, cytotatic, antisthmatic and neuroprotective activities, and is an PTH receptor antagonist. The peptide is useful in the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor. The PTH2 receptor binding activity may be used in treating obesity or other eating or metabolic disorders, mental disorders (e.g. depression, schizophrenia and dementia), acute or chronic pain, migraine or headaches, diabetes and other metabolic disorders, osteoporosis, hypercalcaemia and other disorders affecting calcium metabolism, hypertension, congestive heart failure and control of tumour growth, asthma, emphysema or other restrictive lung diseases, and demyelinating conditions such as multiple sclerosis and leukodystrophies. The present sequence represents a PTH2 receptor which is used in the exemplification of the present invention.

Sequence 546 AA;

Query Match 76.3%; Score 2217.5; DB 22; Length 546;  
Best Local Similarity 76.7%; Pred. No. 5.7e-232;  
Matches 417; Conservative 37; Mismatches 81; Indels 9; Gaps 4;

QY 1 MAMLGASLHWGMLGSLARAQLDSGTITIEQIVLVKAKVQCELNITAOIQEGE 60

Db 1 mpwlealpylgwllirscilvgagldgtlctieeqivlmkkmqncelnltaqfge 60

QY 61 GNCFFPEWGLICWPRGTGKISAVPCPPXYIDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120

Db 61 gncfpewdglicwprtagtsampcpsyvdfnhkgvafhrctpngtwdfhngsnkta 120

QY 121 NYSDCRLFLQPDISGKQECERLYWYVGVISFGSLAVAILLIIGYFRRLHCTRNTH 180

Db 121 nysdc--flqpdinlgkqeffenlyltvgyvisfgslavailliigyfrlrhctrnth 178

QY 181 MHLFVSFMLRATSIYFKDVRVHAHIGVKELESIMDDPQNSEATSVDSKSOYIGCKIAV 240

Db 179 ihlfvsmfmrmsifvkdrvaqahlgvealslvmgdqlqnfiggpsvdkssqyvgckia 238

QY 241 VMFIYFLATNYWILVEGLYHLNLIFVAFSFTKYLWGFILIGWGFPAAFVAAVAVARAT 300  
Db 239 vmfiyflatnywiiwllveglyhlhnlifsvfsfssdkylwgflligwgfpaavfvavavarat 298  
QY 301 LADARCWELSGADKIWIQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRK 360  
Db 299 ladtrcwelsagd-rwiydapilaaiglnfllntvrvlatkiwetnavghdmrkyrk 357  
QY 361 LAKSTLVLVLVFGVHVIVFVCLPHSFTGLGWEIRMHCELFNFSGFVFVSIYCYCNGEV 420  
Db 358 lakstlvlvlvfgvhyivfvcqphsfsglweirmhcelffnsfgfvsivycyngcv 417  
QY 421 QAEVKMMSRWNLSDVMKRTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCLSLAKLPR 480  
Db 418 qaevkktwrnlsidwkappcgghrygsvltvtthstssqsgmgpstrlvliisskpk 477  
QY 481 SPA---DSLTAATSLYLAWSGVQTSRTASHTLSRKNKESGRQRDILMEKFSRPMESNP 537  
Db 478 tacrqldshvtlpgyvwssseqdcqps---tpeetckghgrqeddspvgessrpvafli 534  
QY 538 DTEG 541  
Db 535 dteg 538

RESULT 5

AAV99600

ID AAY99600 standard; Protein; 536 AA.

XX AAY99600;

DT 27-OCT-2000 (first entry)

DE Zebrafish parathyroid hormone type-1 receptor PTH1R.

KW Zebrafish; parathyroid hormone type-1 receptor; PTH1R;

developmental disorder; physiological disorder; neurological disorder.

OS Brachydanio rerio.

PN WO200032775-A1.

PD 08-JUN-2000.

PF 30-NOV-1999; 99WO-US28207.

PR 30-NOV-1998; 98US-0110467.

XX (JUEP/) JUEPPNER H.

PA (RUBI/) RUBIN D A.

PI Jueppner H, Rubin DA;

DR WPI: 2000-412323/35.

DR N-PSDB; AAA49625.

XX New nucleic acids encoding parathyroid hormone receptors PTH1R and PTH3R, useful for treating diseases or disorders associated with impaired receptor functions comprises a specific nucleotide sequence -

PS Claim 17; Fig 2A; 11lpp; English.

XX The present sequence is the parathyroid hormone type-1 receptor (PTH1R) from the zebrafish. Its coding sequence was obtained by sequencing a cDNA clone. The gene and protein can be used to detect diseases in man where the receptor is either overexpressed or underexpressed, and they can be used to treat these diseases, which may be developmental, physiological or neurological disorders. They can also be used to identify agonists and antagonists which can be used in a similar manner. In addition, the gene can be used for chromosome identification.

XX



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SQ Sequence 536 AA;
Query Match 48.8%; Score 1418.5; DB 21; Length 536;
Best Local Similarity 57.8%; Pred. No. 4e-145;
Matches 269; Conservative 80; Mismatches 107; Indels 9; Gaps 6;

QY 4 LGASLHV--WGWLMLGSL-LARAOLDSDGTTTIEQIVLVKAKVQCELNITAQLOEGE 60
DB 1 mgatlvrtlgfllcgtsllsfvgyldavddvltkeeqyllfnakrckeraikshktse 60

QY 61 GNCFFEWGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTTWA 120
DB 1 gscldpewdgilcwpvgpkmvstscpeyiydfnhkhghayrrcdngtwelashhunkwa 120

QY 121 NYSDCRLFLQPDISIGKOEFCERLYVMYTVGYSISFGSLAVAILLIGVFRRLHCTRNYIH 180
DB 121 nysecakffphynqngerevfrlylytvgyislsigslmvatvllgyfrlhcrtnyih 180

QY 181 MHLFVSEMLRATSIKVRVVAHIGVKELESIMODDPQNSIEATSVDKSOYIGCKTAV 240
DB 181 mhlfsfmlraisiivdvlysgsalqemeritv-edlksiteappanktfigckvav 239

QY 241 VMFIYFLATNYWILVEGLYHNLIFVAFPSDTKYLWGFILIGWGFPAFVAWAVARAT 300
DB 240 tlflylatnywvllvegllyhslifmtffsdrkylwgflligwvpmfvtiwasvrat 299

QY 301 LADARCWELSGDIKWYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRK 360
DB 300 ladtecwldisaglnkwilqipiltavvnlflirvatkiretnagrcdtrgqyrk 359

QY 361 LAKSTLVVLVFGVHYIVFVCLPHS-FTGLGWEIRMHCELFNSFGFVSIYCYCNGE 419
DB 360 lkstlvmlpfigvhyivfampytevgvlyqimhyemlfnsvqgffvailyfcnge 419

QY 420 VQAEVKKMWSRWNLSDWKRTPPCGSR--RCGSVL--TTVTHSTS 460
DB 420 vqaeikkawrrtlaldfrkarsgntysyqpmvshstvtnta 464

RESULT 6
AAY90230
ID AAY90230 standard; Protein: 536 AA.
AC AAY90230;
DT 29-AUG-2000 (first entry)
DE Zebrafish PTHr receptor protein sequence.
KW Zebrafish; PTHr receptor; PTH3R receptor; diagnosis: cancer;
KW parathyroid hormone type 1 receptor; parathyroid hormone type 3 receptor.
OS Brachydanio rerio.
PN WO200032771-A1.
PD 08-JUN-2000;
XX 28-MAY-1999; 99WO-US11883.
PR 30-NOV-1998; 98US-0110467.
PA (JUEP/) JUEPNER H.
PA (RUBI/) RUBIN D A.
PI Jueppner H, Rubin DA;
XX WPI: 2000-412319/35.
DR N-PSDB: AAA30828.
XX Novel zebrafish parathyroid hormone/parathyroid hormone related peptide
PT receptor 3 and isolated nucleic acid encoding zebrafish parathyroid
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PT hormone receptor 1 for treating disorders associated with receptor
PT function
XX Claim 17; Fig 2a; l1lpp; English.
PS This sequence is a parathyroid hormone receptor type 1 (PTHr)
XX receptor protein of the invention. The invention also relates to a PTH3R
CC antagonist. Antagonists of PTHr or PTH3R can be used for the
CC treatment of diseases associated with an increase in PTHr or PTH3R
CC activity, respectively. The peptides are used for diagnosis or prognosis
CC of diseases and disorders associated with PTH3R or PTHr, such as cancer.
CC The polypeptides can be used as a molecular weight markers on sodium
CC dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) gels, or
CC on molecular sieve gel filtration columns. Antigenic epitope-bearing
CC peptides and polypeptides are useful to raise antibodies, including
CC monoclonal antibodies, that bind specifically to a polypeptide. The
CC peptides are useful during diagnosis of diseases and disorders in
CC mammals involving PTHr or PTH3R receptor expression or function.
CC Mutations that affect PTHr or PTH3R sequence and/or expression levels
CC of PTHr or PTH3R could be diagnostic for patients with disease or
CC disorders of a developmental, physiological or neurological nature. The
CC nucleic acid molecules are valuable for chromosome identification. The
CC mapping of DNAs to chromosomes is an important first step in
CC correlating those sequences with genes associated with disease.
XX Sequence 536 AA;
SQ
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Query Match 48.8%; Score 1418.5; DB 21; Length 536;
Best Local Similarity 57.8%; Pred. No. 4e-145;
Matches 269; Conservative 80; Mismatches 107; Indels 9; Gaps 6;

QY 4 LGASLHV--WGWLMLGSL-LARAOLDSDGTTTIEQIVLVKAKVQCELNITAQLOEGE 60
DB 1 mgatlvrtlgfllcgtsllsfvgyldavddvltkeeqyllfnakrckeraikshktse 60

QY 61 GNCFFEWGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTTWA 120
DB 1 gscldpewdgilcwpvgpkmvstscpeyiydfnhkhghayrrcdngtwelashhunkwa 120

QY 121 NYSDCRLFLQPDISIGKOEFCERLYVMYTVGYSISFGSLAVAILLIGVFRRLHCTRNYIH 180
DB 121 nysecakffphynqngerevfrlylytvgyislsigslmvatvllgyfrlhcrtnyih 180

QY 181 MHLFVSEMLRATSIKVRVVAHIGVKELESIMODDPQNSIEATSVDKSOYIGCKTAV 240
DB 181 mhlfsfmlraisiivdvlysgsalqemeritv-edlksiteappanktfigckvav 239

QY 241 VMFIYFLATNYWILVEGLYHNLIFVAFPSDTKYLWGFILIGWGFPAFVAWAVARAT 300
DB 240 tlflylatnywvllvegllyhslifmtffsdrkylwgflligwvpmfvtiwasvrat 299

QY 301 LADARCWELSGDIKWYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRK 360
DB 300 ladtecwldisaglnkwilqipiltavvnlflirvatkiretnagrcdtrgqyrk 359

QY 361 LAKSTLVVLVFGVHYIVFVCLPHS-FTGLGWEIRMHCELFNSFGFVSIYCYCNGE 419
DB 360 lkstlvmlpfigvhyivfampytevgvlyqimhyemlfnsvqgffvailyfcnge 419

QY 420 VQAEVKKMWSRWNLSDWKRTPPCGSR--RCGSVL--TTVTHSTS 460
DB 420 vqaeikkawrrtlaldfrkarsgntysyqpmvshstvtnta 464

RESULT 7
AAR92276
ID AAR92276 standard; Protein: 585 AA.
XX AC AAR92276;
XX DT 18-MAY-1996 (first entry)
XX
```

DE Opossum kidney PTH/PTHrP receptor.  
 XX Parathyroid hormone; receptor; parathormone; PTH;  
 KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;  
 KW hypercalcaemia; hypocalcaemia; cancer; opossum.  
 XX Didelphis virginiana.  
 OS US5494806-A.  
 XX 27-FEB-1996.  
 XX 05-APR-1991; 91US-0681702.  
 XX 06-APR-1992; 92US-0864475.  
 PR 05-APR-1991; 91US-0681702.  
 XX (GEO ) GEN HOSPITAL CORP.  
 PA Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;  
 PI Schipani E, Segre GV;  
 XX WPI: 1996-139028/14.  
 DR N-PSDB; AAT15946.  
 XX DNA encoding vertebrate parathyroid hormone receptor - useful for  
 PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,  
 PT cancer etc.  
 XX Claim 1; Fig 2A-2E; 64pp; English.  
 XX Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)  
 CC receptors (AAR92275 and AAR92776) are encoded by cDNA clones OK-H  
 CC (AAT15945) and OK-O (AAT15946), respectively. Isolated from an opossum  
 CC kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2  
 CC separate genes or of a laboratory artifact. The receptor induces an  
 CC increase in intracellular cAMP and calcium when challenged with PTH or  
 CC PTHrP. Recombinant receptors can be produced in vector/host cell systems  
 CC and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia  
 CC and hypocalcaemia, to screen for (ant)agonists and to raise antibodies.  
 CC Host cells expressing the receptor can be used for diagnostic  
 CC measurement of PTH serum levels.  
 XX Sequence 585 AA;

Query Match 47.9%; Score 1392; DB 17; Length 585;  
 Best Local Similarity 47.8%; Pred. No. 3.5e-142;  
 Matches 274; Conservative 92; Mismatches 137; Indels 70; Gaps 9;

QY 24 AQLDSGTTITIEEQIVLVKAKVQCELNITAQLQEGE----- 60  
 Db alvdaddvitkeeqiilllnnaqaqceqrkeivlrpelaesakdmsrsaktkekpaek 83

QY 61 -----GNCPEWDGLCWPRGTGVKISAVPCPPYIYDFNHKGVAFR 101  
 Db lypgaesrevsdrslrldgfcipewdnivcwpagvpgkvavpcpdydfnhkgrayr 143

QY 102 HCNPNGTWDFMHLNKTWANYDCLRFLQPDISIGKQFCERLYVMYTVGYSISFSLAV 161  
 Db rcdsngswelvpgnrtwanyscvkfltnetr--arevfdrlgmitytvgyislsltv 201

QY 162 AILIGVFRRLHCTRNVIHMHFVSEMLRATSIFFVDRVVAHIGVKELESIMQDDPON 221  
 Db avilgyfrlhrctnyihmhlfvsefmlravsfidkavlysgvstdeier-iteelra 260

QY 222 SIATSVDKSYIGCKIAVMFYIATNYWTLVCELYLHNLIFVAFTSDTKYLGWFTL 281  
 Db fteppadkagfvcgvavtvflylfttnyywilvegylhslfmafsekylwgtl 320

QY 282 IGGFFPAFVAANAVARATLADARCHELSAGDIKWYQAPILAAIGLNTFLFLNTYRVLA 341  
 Db fwglpavfvavvwtvratlantecwdlssgnkklwlpilaavvntflfinirvia 380

QY 342 TKIWETNAVGHDTKQYRKLAQKSTLVLVFGVHYIVFVCLPHS-FTGLGWETRMHCELF 400  
 Db tkiretnagrcdrqyrklkltstvlmpfghyivfmatpytevsgilwqvmhyeml 440

QY 401 FNSFQGFVSIYCYCNGEVQAEVKKMSRWNLSDVMKRTPCGSGRRCGSVLTVTTH--- 457  
 Db fnsfggfvaliycfngcvqaeikksrwrtlaldfrkrksrgs-----stysyggpm 493

QY 458 -STSSQSVAAAHAWCLSLAKLPSPADSLTATSLYLAMSGVTQSTASHTLSTRNKED 516  
 Db vhtsvtnvgprggialsls--prlapgagasanghhqipygvykhsisen-slpesgpe 550

QY 517 SGRQRDDILM-----EKPSRPESNPDT 539  
 Db pgtkddgyingsglyepmvggeqppplleeret 583

RESULT 8  
 AAW73315  
 ID AAW73315 standard; Protein; 585 AA.  
 XX AC AAW73315;  
 XX DT 08-FEB-1999 (first entry)  
 XX DE Parathyroid hormone receptor OK-O.  
 XX KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;  
 KW PTH-related hypercalcaemia; opossum.  
 XX OS Didelphis virginiana.  
 XX PN US5840853-A.  
 XX PD 24-NOV-1998.  
 XX PF 06-JUN-1995; 95US-0471494.  
 XX PR 06-APR-1992; 92US-0864475.  
 PR 05-APR-1991; 91US-0681702.  
 PR 06-JUN-1995; 95US-0471494.  
 XX (GEO ) GEN HOSPITAL CORP.  
 XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;  
 PI Schipani E, Segre GV;  
 XX WPI: 1999-0341124/03.  
 DR N-PSDB; AAV08389.  
 XX Antibody to parathyroid hormone receptor - for diagnostic or  
 PT therapeutic use  
 XX Claim 6; Fig 2; 63pp; English.  
 XX This sequence represents the opossum parathyroid hormone (PTH) receptor  
 CC OK-O, which is targeted by the antibody of the invention. The antibody  
 CC of the invention is immunoreactive with naturally occurring human, rat or  
 CC opossum PTH receptor. The antibody is useful for treating disorders  
 CC characterised by overstimulation of PTH receptors by their ligand and for  
 CC the diagnosis of PTH-related hypercalcaemia.  
 XX Sequence 585 AA;

Query Match 47.9%; Score 1392; DB 20; Length 585;  
 Best Local Similarity 47.8%; Pred. No. 3.5e-142;  
 Matches 274; Conservative 92; Mismatches 137; Indels 70; Gaps 9;

QY 24 AQLDSGTTITIEEQIVLVKAKVQCELNITAQLQEGE----- 60  
 Db alvdaddvitkeeqiilllnnaqaqceqrkeivlrpelaesakdmsrsaktkekpaek 83

Qy	61	-----GNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHHGVAFR	101
Db	84	lypqaeesrevsdrslqdgfcelpcedwnivcwpagvgkvvavpcpdyfydfnhkgrayr	143
Qy	102	HCNPNGTWDPMHSLNKTWANYSDCLRFLOPDISIGKQFCERLYVMYTVGVSYSPGSLAV	161
Db	144	rcdsngswelvpgnntwtanysecvfltnetr--erevdfrlgmlytvgvyslsgstcv	201
Qy	162	AILIIGYFRLHCHTRNYIHMHLFVSPMLRATSIYFKVDRVVHAHIGVKELESIMODDPQN	221
Db	202	avilygyfrrlchtrnyihmhlfvsmrlravslfkdavlysgvstdeier-iteeelra	260
Qy	222	SIEATSVDRSQYIGCKIANYMFTYFIATNYWILVEGLYHNLIFVAPSPDTKYLWGFIL	281
Db	261	ftepppadkagfvgcwavtvflyfittnywilyveglyhslifmaffsekkyigwftl	320
Qy	282	IGMGFFAAVFAAVAVARATLADARCWELSGADIKWTYQAPILAAATGLNFIPLNTVRVLA	341
Db	321	fwglpavfavvwtvratlantecwdlsgnkkwliqvpilaalvvnfilfiniirvla	380
Qy	342	TKIWTENAVGHDPKQYRKLAKSTLVLVFVGWHYIYFVCLPHS-FTGLGWIRHMCELF	400
Db	381	tklirenagrcdtrqgyrkllkxstlvmpflgvyhyivmatpytevsgilwqvmghyeml	440
Qy	401	FNSEQCFEYSIIYCYCNGEVQAEVKWWSRNLSVDWKETPCGSRRCGSVLITVTH--	457
Db	441	fnsfqgffvallyfcngevqaeikswsrwtlaldfrkarsgs-----stysyqpm	493
Qy	458	-SPSSQSOVAAAHAHWCLSLAKLIPRSPADSLTATSLYLAMSGVQTSRTASHTLSITSNKED	516
Db	494	vshtstvnvpgpglalsis--prlapgagasanghqlpgvykhsisen-slpssgpe	550
Qy	517	SGRQRDDILM-----EKPSRPMESNPDT	539
Db	551	pqtckdqyinqsdlvepmvgvcppllleceerf	583

RESULT 9  
AAR27705  
ID AAR27705 standard; Protein; 585 AA.

AA AAR27705; AC

DT 16-MAR-1993 (first entry)

DE Opossum kidney pTH/PTHrP receptor prod. from clone OK-0.

AA  
KW Parathyroid hormone; related protein; calcium; antagonist;  
KW antibodies; hypercalcaemia.

XX  
OS  
Didelphis virginiana.

XX PN WO9217602-A.

XX 15-OCT-1992.  
PD

AA 06-APR-1992; 92WO-US02821.  
PF

AA 05-APR-1991; 91US-0681702.

PR 00-APR-1992; 9205-08044/3.  
XX

PA (GEHO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.

PI Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E; PI Segre GV;

WPI: 1992-366271/44.

DR N-PSDB; AAQ29605.

New DNA encoding parathyroid hormone receptor, DNA and antibodies  
- for (differential) diagnosis of hypercalcaemia, and diagnosis  
and treatment of tumours

Disclosure; Fig 2; 9lpp; English.

The parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP) receptor protein sequence was deduced from the DNA sequence of the clone OK-O, isolated from opossum kidney (OK) cells. The clone OK-O is identical to the OK-H clone except at the C-terminal tail as OK-O encodes a 585 amino acid protein, OK-H encodes one of 515 amino acids. The difference is attributed to a single nucleotide deletion in the OK-H sequence causing a frame shift and an earlier stop codon. It is not known whether OK-O and OK-H represent prods. of two separate genes or are a laboratory artifact. The protein may be used in a therapeutic compsn. to inhibit activation of PTH or PTHrP and thus reduce the level of calcium in the blood. Cpsds. capable of competing with PTH or PTHrP for binding can be identified using the protein prod. and DNAs homologous to PTH DNA can be identified using fragments of the clone as probes. The sequence may be used for the prodn. of antibodies useful for the treatment, classification, prognosis and/or treatment of disorders related to the interaction between a cell receptor and a ligand such as in hypercalcaemia. See also AAR27704-16.

Sequence 585 AA;

Query Match 47.9%; Score 1391; DB 13; Length 585;  
Best Local Similarity 47.8%; Pred. No. 4.5e-142;  
Matches 274; Conservative 93; Mismatches 136; Indels 70; Gaps 10;

Qy	24	AQLDSOGTITIEQIVLVLKAKVOCELNIT	53
Db	24	alvdadvitkeeqiillrnaaqaceqrk	83
Qy	54	--AQLOEG-----EGNCPEWDGLICWPGT	10
Db	84	lypqaeesrevsdrlqdqgclpewdnvcwpgagvkv	14
Qy	102	HCPNCTWDFMHSLNKNTWANTSDCLRFLOPDISIG	16
Db	144	rcdngswelvgpnnrtwanyscecvkfltnetr--	20
Qy	162	AILIICYFRLRHCTRNYTHMHLFVSFMLRATPSF	22
Db	202	avilyfrrlchtrcnymhmlfvsmfmravsfikd	26
Qy	222	SIATSVDSKSOVIGCKIAVMFIFELATNYWILVE	28
Db	261	fteppadkagfvgrvavtvlftltnywyllvegl	32
Qy	282	IGWGFPAAFVAWAVARATLADARCWELSGADIK	34
Db	321	fwgwpavfvavvtratlantecwdlssgnkwiq	38
Qy	342	TKIWTETNAVGHTRKOYRKRLAKSTLVLVFP	40
Db	381	tklirecnagrcdggqrklkstkstlmpfgvhy	44
Qy	401	FNSFOGFFVSIYCYCNEGVEQAEVKKWMSRNL	45
Db	441	fnsqgfvraillyfcngvgeaelkswrwlclaid	49
Qy	458	-STSSOSQVAAAAHACLSLAKLRPSADSLTAT	51
Db	494	vshtsvtnvgprggialsls--prlapagagas	55
Qy	517	SGRQRDILM-----EKPSRPMSNPDT	539
Db	551	pqtckddqylnqsqlvepmvqecppllleeeret	583

RESULT 10  
AAR92275  
ID AAR92275 standard; Protein; 515 AA.  
XX

[illegible]

\_\_\_\_\_

may be used for the production of antibodies useful for the treatment of the clone as probes. The protein

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XX A rat parathyroid hormone/parathyroid hormone-related protein  
 CC (PTH/PTHrP) receptor (AAR92277) is encoded by cDNA clone R15B  
 CC (AA715947) isolated from a rat osteosarcoma ROS 17/2.8 cDNA library.  
 CC The receptor is a G-protein linked receptor having 7 transmembrane  
 CC domains. It induces an increase in intracellular cAMP and calcium  
 CC upon challenge with PTH or PTHrP. Recombinant receptor can be  
 CC produced in vector/host cell systems and used in the treatment,  
 CC diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia,  
 CC to screen for (ant)agonists and to raise antibodies. Host cells  
 CC expressing the receptor are used for diagnostic measurement of PTH  
 CC serum levels.  
 XX SQ Sequence 591 AA;

Query Match 45.8%; Score 1331.5; DB 17; Length 591;  
 Best Local Similarity 46.6%; Pred. No. 1.4e-135;  
 Matches 270; Conservative 86; Mismatches 136; Indels 87; Gaps 11;

QY 22 ARAQLSDGTITIEQIVLVKAKVOCE-----LNITAQLOEGEGN----- 62  
 DB 22 ayalvdaddvftkeeqifilhraaqcdkllkevlhtaanimeskgtwtpastsgkprke 81  
 QY 63 -----CFPEWDGLICWPRGTGKISAVPCPPYIYDFNHK 96  
 DB 82 kasgkfypeskenkdvtgsrrrrgpcldpewdnivcplgaggevvavpcpdyiydfnhk 141  
 QY 97 GVAFRHCNPGTWDFMHSLNKWTANYSDCLRFLOPDISIGKQFCERLYVMYTVGYSISF 156  
 DB 142 ghayrrcdngswewvpgnhrtwanyseclkmtnetr--erevdrfmglytvgymsl 199  
 QY 157 GSLAVAILIIGFRRLLHCTRNTHMHLFVSFMLRATSIKVRVVAHIGVKELES--- 213  
 DB 200 asltvavilaylfrlhrctnrnyhbmflsmlraasifvkdavysgftldeaeerltee 259  
 QY 214 ----IMQDDPQNSIEATSDKSOYIGCKTAVVMFYIFLATNYWILVEGLYLHNLIFVAF 269  
 DB 260 elhiatqvpvpppaaavg-----yagcrvavtfflylatnywvllvegllyhslifmaf 314  
 QY 270 FSDTKYLWGFILIGWGFPAFVAANAVARATLADARCWELSGADIKWIYQAPILAAIGLN 329  
 DB 315 fsekylwgtftifgwglpavvavvgratiantgcwldssghkwiqvillasvln 374  
 QY 330 FILELNTVRLATKWTETNAVGHDRKQYKLAQSTLVLLVFGVHYIVFVCLPHS-FTG 388  
 DB 375 filfinilrvlatkiretnagrcdtrqyrkllrstlrvlplfgvhytvmalpytevsg 434  
 QY 389 LGWEIRMHCELFNFSGQFFVSIYCYCNGEVOAEVKMWRNLSVDWKRTPPCGSRRC 448  
 DB 435 tlwqmqmhyemlfnsfggfvaliycfcngvqaeirksrwtaldfkrkarsgssy 494  
 QY 449 GSVLTVTHSTSSQSOVAAAHAWCLSLAKLPRSPADSLTATSLYLAMSG-----VTQS 501  
 DB 495 -sygpmvshstsvtnvprag----lslpsrlpp---attnghsqldpghakpgapatet 546  
 QY 502 RTASHTLSRS-----NKEDSGRQRDDILMEK 528  
 DB 547 eltpvmtavpkddgflngscsgldaeasgsarpppllqe 585

RESULT 15  
 ID AA773316  
 ID AA773316 standard; Protein; 591 AA.  
 XX AA773316;  
 AC AA773316;  
 XX 08-FEB-1999 (first entry)  
 XX Parathyroid hormone receptor R15B.  
 DE Parathyroid hormone receptor; PTH receptor; antibody; therapy;  
 KW PTH-related hypercalcaemia; rat.

XX Rattus sp.  
 OS US5840853-A.  
 PN 24-NOV-1998.  
 PD 06-JUN-1995; 95US-0471494.  
 PF 06-APR-1992; 92US-0864475.  
 PR 05-APR-1991; 91US-0681702.  
 PR 06-JUN-1995; 95US-0471494.  
 XX (GEO) GEN HOSPITAL CORP.  
 XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;  
 PI Schipani E, Segre GV;  
 XX WPI; 1999-034124/03.  
 DR N-PSDB; AAV08390.  
 XX Antibody to parathyroid hormone receptor - for diagnostic or  
 PT therapeutic use  
 PS Claim 6; Fig 3; 63pp; English.  
 XX This sequence represents the rat parathyroid hormone (PTH) receptor  
 CC R15B, which is targeted by the antibody of the invention. The antibody  
 CC of the invention is immunoreactive with naturally occurring human, rat or  
 CC opossum PTH receptor. The antibody is useful for treating disorders  
 CC characterised by overstimulation of PTH receptors by their ligand and for  
 CC the diagnosis of PTH-related hypercalcaemia.  
 XX SQ Sequence 591 AA;

Query Match 45.8%; Score 1331.5; DB 20; Length 591;  
 Best Local Similarity 46.6%; Pred. No. 1.4e-135;  
 Matches 270; Conservative 86; Mismatches 136; Indels 87; Gaps 11;

QY 22 ARAQLSDGTITIEQIVLVKAKVOCE-----LNITAQLOEGEGN----- 62  
 DB 22 ayalvdaddvftkeeqifilhraaqcdkllkevlhtaanimeskgtwtpastsgkprke 81  
 QY 63 -----CFPEWDGLICWPRGTGKISAVPCPPYIYDFNHK 96  
 DB 82 kasgkfypeskenkdvtgsrrrrgpcldpewdnivcplgaggevvavpcpdyiydfnhk 141  
 QY 97 GVAFRHCNPGTWDFMHSLNKWTANYSDCLRFLOPDISIGKQFCERLYVMYTVGYSISF 156  
 DB 142 ghayrrcdngswewvpgnhrtwanyseclkmtnetr--erevdrfmglytvgymsl 199  
 QY 157 GSLAVAILIIGFRRLLHCTRNTHMHLFVSFMLRATSIKVRVVAHIGVKELES--- 213  
 DB 200 asltvavilaylfrlhrctnrnyhbmflsmlraasifvkdavysgftldeaeerltee 259  
 QY 214 ----IMQDDPQNSIEATSDKSOYIGCKTAVVMFYIFLATNYWILVEGLYLHNLIFVAF 269  
 DB 260 elhiatqvpvpppaaavg-----yagcrvavtfflylatnywvllvegllyhslifmaf 314  
 QY 270 FSDTKYLWGFILIGWGFPAFVAANAVARATLADARCWELSGADIKWIYQAPILAAIGLN 329  
 DB 315 fsekylwgtftifgwglpavvavvgratiantgcwldssghkwiqvillasvln 374  
 QY 330 FILELNTVRLATKWTETNAVGHDRKQYKLAQSTLVLLVFGVHYIVFVCLPHS-FTG 388  
 DB 375 filfinilrvlatkiretnagrcdtrqyrkllrstlrvlplfgvhytvmalpytevsg 434  
 QY 389 LGWEIRMHCELFNFSGQFFVSIYCYCNGEVOAEVKMWRNLSVDWKRTPPCGSRRC 448  
 DB 435 tlwqmqmhyemlfnsfggfvaliycfcngvqaeirksrwtaldfkrkarsgssy 494  
 QY 449 GSVLTVTHSTSSQSOVAAAHAWCLSLAKLPRSPADSLTATSLYLAMSG-----VTQS 501

Db 495 -sygmvshtsvtnvprag----lslpsrlpp---atnghsqipghakpgapatet 546  
Qy 502 RTASHTLSTRS-----NKEDSGRQDDILMEK 528  
Db 547 etlpvtnavpkddgflngscsgldeasgsarpppliqe 585

Search completed: September 21, 2001, 17:05:44  
Job time: 828 sec



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OM protein - protein search, using sw model

Run on: September 21, 2001, 16:53:22 ; Search time 19.54 Seconds  
(without alignments)  
2109.029 Million cell updates/sec

Title: US-09-236-468a-2  
Perfect score: 2907  
Sequence: 1 MAWLGLASLHVWGLMLGSL.....DDILMEKPSRPMESNPDTG 541

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2635	90.6	550	2 A57519	parathyroid hormon
2	1392	47.9	585	2 A39286	parathyroid hormon
3	1336.5	46.0	593	2 A49191	parathyroid hormon
4	1331.5	45.8	591	2 I34195	parathyroid hormon
5	1324	45.5	591	2 S44203	parathyroid hormon
6	1298.5	44.7	589	2 I59297	parathyroid hormon
7	801	27.6	449	2 S16319	secretin receptor
8	776	26.7	440	2 JC2532	secretin receptor
9	772.5	26.6	459	2 JH0594	vasoactive intesti
10	756	26.0	460	2 JC2194	vasoactive intesti
11	755.5	26.0	495	2 JC2195	vasoactive intesti
12	713.5	24.5	437	2 JU0185	PACAP/VIP receptor
13	708	24.4	437	2 S39069	vasoactive intesti
14	702	24.1	438	2 G02822	vasoactive intesti
15	696.5	24.0	467	2 JN0616	pituitary adenylat
16	689.5	23.7	525	2 JN0902	pituitary adenylat
17	682.5	23.5	495	2 S39061	pituitary adenylat
18	681.5	23.4	495	2 S36114	pituitary adenylat
19	673.5	23.2	513	2 S47631	pituitary adenylat
20	667.5	23.0	523	2 S39060	pituitary adenylat
21	662	22.8	462	2 JC2462	gastric inhibitory
22	655	22.5	463	2 A46172	glucagon-like pept
23	641.5	22.1	466	2 G02234	gastric inhibitory
24	641.5	22.1	466	2 S66676	glucose-dependent
25	630.5	21.7	463	2 I84494	glucagon-like pept
26	628.5	21.6	423	2 A45363	somatoliberin rece
27	620.5	21.3	463	2 S71624	glucagon-like pept
28	619	21.3	477	2 JC2041	glucagon receptor
29	618.5	21.3	381	2 S33449	pituitary adenylat

ALIGNMENTS

RESULT 1

A57519 parathyroid hormone receptor 2 precursor - human

N:Alternate names: PTH2 receptor

C:Species: Homo sapiens (man)

C>Date: 08-Dec-1995 #sequence\_revision 08-Dec-1995 #text\_change 24-Nov-1999

C:Accession: A57519

R:Usdin, T.B.; Gruber, C.; Bonner, T.I.

J. Biol. Chem. 270, 15455-15458, 1995

A:Title: Identification and functional

A:Reference number: A57519; MUID:95318121

A:Accession: A57519

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-350 <DS>

A:Cross-references: GB:U25128; NID:g887966; PIDN:AAC50157.1; PID:g887967.

C:Genetics:

A:Gene: GDB:PTH2R2; PTHR2R

A:Cross-references: GDB:731977; OMIM:601469

A:Map position: 2q33-2q33

C:Superfamily: glucagon receptor

C:Keywords: hormone receptor

Query Match 90.6%; Score 2635; DB 2; Length 550;  
Best Local Similarity 91.4%; Pred. No. 8.6e-214;  
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;

QY	1	MAWLGLASLHVWGLMLGSCLLARAQLDSGDTITIEQIVLVLKAKVQCELNITAQLOEGE	60
DB	1	MAGLGLASLHVWGLMLGSCLLARAQLDSGDTITIEQIVLVLKAKVQCELNITAQLOEGE	60
QY	61	GNCFPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCPNPNGTWDFHSLNKTWA	120
DB	61	GNCFPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCPNPNGTWDFHSLNKTWA	120
QY	121	NYSDCLRFLOPDISICKQEFCEERLYVMYTVGVYSISFGSLAVAILLIIGYFRLHCTNYIH	180
DB	121	NYSDCLRFLOPDISICKQEFCEERLYVMYTVGVYSISFGSLAVAILLIIGYFRLHCTNYIH	180
QY	181	MHLFVSFMLRATSIKVDKRVVHAHIGVKELESIMODDPQNSIEATSVDKSOYIGCKIAV	240
DB	181	MHLFVSFMLRATSIKVDKRVVHAHIGVKELESIMODDPQNSIEATSVDKSOYIGCKIAV	240
QY	241	VMFIYFLATNYWILVEGLYLHNLIJFVAFSDTKYLMGFILIGWGFPAFVAWAVARAT	300
DB	241	VMFIYFLATNYWILVEGLYLHNLIJFVAFSDTKYLMGFILIGWGFPAFVAWAVARAT	300
QY	301	LADARCWELSGADIKWIYQAPILAAIGLFIPLFNTVRVLATKIWETNAVGHDTKQYRK	360
DB	301	LADARCWELSGADIKWIYQAPILAAIGLFIPLFNTVRVLATKIWETNAVGHDTKQYRK	360





A;Residues: 1-440 <JIA>

449 GSVLTITVTHSTSSQSQVAHAHAWCLSLAKLPR 480

A:Accession: JC2194  
A:Molecule type: mRNA  
A:Residues: 1-460 <COU>  
A:Cross-references: EMBL:X75299; NID:g407461; PID:CAA53046.1; PID:g407462  
A:Experimental source: jejunal epithelial cell; clone h1VR8  
R:Sreedharan, S. P.; Patel, D. R.; Huang, J. X.; Goetzl, E. J.  
Biochem. Biophys. Res. Commun. 193, 546-553, 1993  
A:Title: Cloning and functional expression of a human neuroendocrine vasoactive  
A:Reference number: JN0604; MUID:93290641  
A:Accession: JN0604  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-284,288-460 <SRE>  
A:Cross-references: GB:I13288; NID:g292903; PID:AAA36805.1; PID:g292904  
R:Coûvaineau, A.; Gaudin, P.; Maoret, J. J.; Rouvier-Fessard, C.; Nicolle, P.; Labau-

RESULT 12











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OM protein - protein search, using sw model

Run on: September 21, 2001, 17:05:47 ; Search time 13.2 seconds  
(without alignments)  
1403.956 Million cell updates/sec

Title: US-09-236-468a-2

Perfect score: 2907

Sequence: 1 MAWLGAHLHWGWLMLGSL.....DDILMEKSRPMESNPDTG 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2635	90.6	550	1 PTR2_HUMAN	P49190 homo sapien
2	2213.5	76.1	546	1 PTH2_RAT	P70555 rattus norv
3	1397	48.1	585	1 PTRR_DIDMA	P25107 didelphis m
4	1345	46.3	585	1 PTRR_PIG	P50133 sus scrofa
5	1336.5	46.0	593	1 PTRR_HUMAN	Q03431 homo sapien
6	1331.5	45.8	591	1 PTRR_RAT	P25961 rattus norv
7	1324	45.5	591	1 PTRR_MOUSE	P41593 mus musculus
8	801	27.6	449	1 SCRC_RAT	P38111 rattus norv
9	794	27.3	445	1 SCRC_RABIT	O46502 oryctolagus
10	785	27.0	458	1 VIPR_PIG	Q28992 sus scrofa
11	784	27.0	440	1 SCRC_HUMAN	P47872 homo sapien
12	782	26.9	447	1 VIPR_CARAU	Q90308 carassius a
13	772.5	26.6	459	1 VIPR_RAT	P30083 rattus norv
14	759.5	26.1	457	1 VIPR_HUMAN	P32241 homo sapien
15	713.5	24.5	437	1 VIPS_MOUSE	P41588 mus musculus
16	708	24.4	437	1 VIPS_RAT	P35000 rattus norv
17	702	24.1	438	1 VIPS_HUMAN	P41587 homo sapien
18	685	23.6	468	1 PACR_HUMAN	P41586 homo sapien
19	677.5	23.3	496	1 PACR_MOUSE	P70205 mus musculus
20	673.5	23.0	513	1 PACR_BOVIN	Q29627 bos taurus
21	667.5	23.0	523	1 PACR_RAT	P32215 rattus norv
22	665	22.9	550	1 GLP2_RAT	Q36040 rattus norv
23	663	22.8	489	1 GLP1_MOUSE	Q35659 mus musculus
24	662	22.8	462	1 GIPR_MESAU	P43218 mesocricetu
25	655	22.5	463	1 GLP1_RAT	P32301 rattus norv
26	641.5	22.1	466	1 GIPR_HUMAN	P48546 homo sapien
27	635.5	21.9	553	1 GLP2_HUMAN	Q95838 homo sapien
28	630.5	21.7	423	1 GRFR_HUMAN	Q02643 homo sapien
29	628.5	21.6	463	1 GLP1_HUMAN	P43220 homo sapien
30	622.5	21.4	423	1 GRFR_PIG	P34999 sus scrofa
31	619	21.3	477	1 GLR_HUMAN	P47871 homo sapien
32	616	21.2	455	1 GIPR_RAT	P43219 rattus norv
33	607	20.9	485	1 GLR_RAT	P30082 rattus norv

## RESULT 1

## PTR2\_HUMAN

## ID

## PTR2\_HUMAN

## STANDARD;

## PRT;

## 550 AA.

## AC

## P49190;

## DT

## 01-FEB-1996

## (Rel. 33, Created)

## DT

## 01-FEB-1996

## (Rel. 33, Last sequence update)

## DT

## 01-OCT-2000

## (Rel. 40, Last annotation update)

## DE

## PARATHYROID HORMONE RECEPTOR PRECURSOR (PTH2 RECEPTOR).

## GN

## PTH2.

## OS

## Homo sapiens (Human).

## OC

## Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## OC

## Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## OX

## NCBI\_TaxID=9606;

## RN

## (1)

## SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

## RP

## TISSUE=Brain;

## RX

## MEDLINE=95318121; PubMed=7797535;

## RA

## Urdin T.B., Gruber C., Bonner T.I.;

## RT

## "Identification and functional expression of a receptor selectively

## recognizing parathyroid hormone, the PTH2 receptor.";

## RT

## J. Biol. Chem. 270:15455-15458(1995).

## RN

## (2)

## SEQUENCE OF 26-40 AND 306-550 FROM N.A.

## RX

## MEDLINE=97079671; PubMed=8921382;

## RA

## Urdin T.B., Modi W., Bonner T.I.;

## RT

## "Assignment of the human PTH2 receptor gene (PTH2) to chromosome 2q33

## by fluorescence in situ hybridization.";

## RL

## Genomics 37:140-141(1996).

## CC

## -1- FUNCTION: THIS IS A SPECIFIC RECEPTOR FOR PARATHYROID HORMONE. THE

## ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE

## ADENYL CYCLASE.

## CC

## -1- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN BRAIN AND PANCREAS.

## CC

## ALSO EXPRESSED IN THE TESTIS.

## CC

## -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

## CC

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## CC

## EMBL; U25128; AAC50157.1; -

## DR

## EMBL; U47124; AAA96796.1; -

## DR

## EMBL; U47129; AAC50767.1; -

## DR

## EMBL; U47125; AAC50767.1; JOINED.

## DR

## EMBL; U47126; AAC50767.1; JOINED.

## DR

## EMBL; U47127; AAC50767.1; JOINED.

## DR

## EMBL; U47128; AAC50767.1; JOINED.

## DR

## GCRdb; GCR 2003; -

## DR

## MIM; 601469; -

## DR

## InterPro; IPR000832; -

## DR

## Pfam; PF00002; 7tm.2; 1.

## DR

## PRINTS; PR00249; GPCRSECRETIN.

## DR

## PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.



Best Local Similarity 76.5%; Pred. No. 8.5e-164;		Matches 416; Conservative 37; Mismatches 82; Indels 9; Gaps 4;	
QY	1	MAWLASLHWGMLGSCLLARAOQSDGTITIEEQIVLVKAKVOCELNITAOQEGE	60
Db	1	MPWLEALPYGWLILRLSCVLGAQSDGTITIEEQIVLVKAKVOCELNITAOQEGE	60
QY	61	GNCFPDGLICPRGTGKISAVPCPPXYIYDFNHRGVAFRHCPNPNGTWDFMHSNKTWA	120
Db	61	GNCFPDGLICPRGTAGKTAMPSPSYVDYFNHKGVAFRHCTPNTWDFIHGSKNTWA	120
QY	121	NYSDCRLFPQDISKQCEFCERLYVMYVGVYSISFGSLAVAILIIGYFRRLHCTRYIH	180
Db	121	NYSDC--FLQPDINIGKQEFFENLYIYTVGVYSISFGSLAVAILIIGYFRRLHCTRYIH	178
QY	181	MHLFVSMRLRATSIYFKVDRVVAHIGVKELESIMODDPONSTEATSVDKSOYIGCKIAV	240
Db	179	LHLFVSMRLRATSIYFKVDRVVAHIGVKELESIMODDPONSTEATSVDKSOYIGCKIAV	238
QY	241	VMIYFELATNYWILVEGLYLHNLIFVAFSDTKYLMGFFILIGWGFPAAFVAAWAVARAT	300
Db	239	VMIYFELATNYWILVEGLYLHNLIFVAFSDTKYLMGFFILIGWGFPAFVAAWAVARAT	298
QY	301	LADARCWELSGADIKWYQAPILAAATGLNFIPLNTRVRLATKINETNAVGHDRKOYRK	360
Db	299	LADTRCWELSGAD--RWYXXPILAAATGLNFIPLNTRVRLATKINETNAVGHDRKOYRK	357
QY	361	LAKSTLVLVGVHIVFVCLPHSTGLGWELRMHCELFNFSQGFVYIYCYNGEV	420
Db	358	LAKSTLVLVGVHIVFVCLPHSTGLGWELRMHCELFNFSQGFVYIYCYNGEV	417
QY	421	QAEVKMWRNLSDVWKRTPPCGSRGCVLTVTTHSTSSQVAAAHAWCLSLAKLPR	480
Db	418	QAEVKKTWRNLSDVWKRTPPCGSRGCVLTVTTHSTSSQVAAAHAWCLSLAKLPR	477
QY	481	SPA--DSITATSLYLAHSVQTSRTASHTLSRNSKSGRQDDILMEKSPRPESNP	537
Db	478	TACRQIDSHVTLPGYVWSSSEQDCQPS---TPTEETKKGROEDDSPVGESSRPVAFRI	534
QY	538	DTEG 541	
Db	535	DTEG 538	
RESULT 3			
PTRR DIDNA			
AC	PTRR DIDNA	STANDARD;	PRT; 585 AA.
DT	P25107;		
DT	01-MAY-1992 (Rel. 22, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR		
DE	PRECURSOR (PTH/PTHR RECEPTOR).		
GN	PTHR.		
OS	Didelphis marsupialis virginiana (North American opossum).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.		
OX	NCBI_TaxId=9267;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=92054592; PubMed=1658941;		
RA	Jueppner H., Abou-Sanra A.-B., Freeman M., Kong X.-F., Schipani E.,		
RA	Richards J., Kolekowsky L.F. Jr., Hock J., Potts J.T. Jr.,		
RA	Kronenberg H.M., Segre G.V.;		
RT	"A G protein-linked receptor for parathyroid hormone and parathyroid		
RT	hormone-related peptide."		
RL	Science 254:1024-1026(1991).		
CC	-!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR		
CC	PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS		
CC	RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL		
CC	CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER		
CC	SYSTEM.		
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.		
-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.			
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the European Bioinformatics Institute. There are no restrictions on its			
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modified and this statement is not removed. Usage by and for commercial			
entities requires a license agreement (See http://www.isb-sib.ch/announce/			
or send an email to license@isb-sib.ch).			
CC	EMBL; M74445; AAA30979.1; -		
CC	PIR; A39286; A39286.		
CC	GCRdb; GCR_0204; -		
CC	InterPro; IPR000832; -		
CC	InterPro; IPR002170; -		
CC	Pfam; PF00002; 7tm_2; 1		
CC	PRINTS; PR00249; GPCRSECRETIN.		
CC	PRINTS; PR00393; PTRHORMONER.		
CC	PROSITE; PS00649; G-PROTEIN_RECEP_F2_1; 1.		
CC	PROSITE; PS00650; G-PROTEIN_RECEP_F2_2; 1.		
CC	PROSITE; PS0227; G-PROTEIN_RECEP_F2_3; 1.		
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.		
FT	SIGNAL 1 26		
FT	CHAIN 27 585		
FT	PARATHYROID HORMONE/PARATHYROID HORMONE-		
FT	RELATED PEPTIDE RECEPTOR.		
FT	EXTRACELLULAR (POTENTIAL).		
FT	DOMAIN 27 185		
FT	TRANSMEM 186 209		
FT	DOMAIN 210 216		
FT	TRANSMEM 217 236		
FT	DOMAIN 237 276		
FT	TRANSMEM 277 300		
FT	DOMAIN 301 314		
FT	TRANSMEM 315 336		
FT	DOMAIN 337 355		
FT	TRANSMEM 356 376		
FT	DOMAIN 377 403		
FT	TRANSMEM 404 422		
FT	DOMAIN 423 434		
FT	TRANSMEM 435 457		
FT	DOMAIN 458 585		
FT	CARBOHYD 148 148		
FT	CARBOHYD 158 158		
FT	CARBOHYD 163 163		
FT	CARBOHYD 173 173		
SQ	SEQUENCE 585 AA; 65963 MW; 34900384CD6DF477 CRC64;		
Query Match 48.1%; Score 1397; DB 1; Length 585;			
Best Local Similarity 48.0%; Pred. No. 1.1e-100;			
Matches 275; Conservative 94; Mismatches 134; Indels 70; Gaps 10;			
QY	24	AQLSDGTTITIEQIVLVKAKVOCELNIT	53
Db	24	ALVDDVITTKEQIILLRNAQACEQLKEVLRVPELAESAADMWRSRKTKEKPAEK	83
QY	54	--AQLEQ-----EGNCFPEWDGLICPRGTGKISAVPCPPYIYDFNHRGVAFR	101
Db	84	LYSQAESREVSDRSRLQDGFCLPEWDNIVCNPAGVPGKVVAVPCPDYIYDFNHRGVAFR	143
QY	102	HCPNPGTDFMHSNKTWANYSDCLRFQPDISIGICEFCERLYVMYVGVYSISFGSLAV	161
Db	144	RCDNSGWSWELVPGNRTWANYSECVKFLNETR--EREVDFRLGMIYTVGVYSISGLSLV	201
QY	162	AILIIGYFRRLHCTRYIHMHLPVSMRLRATSIYFKVDRVVAHIGVKELESIMODDPON	221
Db	202	AVLIGYFRRLHCTRYIHMHLPVSMRLRATSIYFKVDRVVAHIGVKELESIMODDPON	260
QY	222	STEATSVDRSQYIGCKIAVVMFYFLATNYWILVEGLYLHNLIFVAFSDTKYLMGFFIL	281
Db	261	FTEPPADKAGVGCVRVAVTVFLTYTYWILVEGLYLHSLIFNAFFSEKYLGMGFTL	320
QY	282	IGWGFPAFVAAWAVARATLADARCWELSGADIKWYQAPILAAATGLNFIPLNTRVRLA	341

Db 321 FGGLPAVFAVVMVTVRATIANTECHDNLSSGNKKWIIQVPIILAAIVVNFILFINIRVLA 380  
QY 342 TKIETNAVGHDRKQYKRLAKSTLVLFVGVHYIVFVCLPHS-FTGLGWEIRMHCELF 400  
Db 381 TKLRETNAGRCDFRQYKLLKSTLVLMPLFGVHYIVFMATPYTEVSGILMVQVMHYEML 440  
QY 401 FNSFGFFVYIIYCYCNGEVOAEVKKMWSRNLSVDMKRPVPCGSRRCGSLVLTVTTH--- 457  
Db 441 FNSFGFFVYIIYCYCNGEVOAEIKKWSRWTLALDFKRRKARSGS-----STYSYGP 493  
QY 458 -STSSQVAAAHAWCLSLAKLSPSPADSLTATSLYLAWSGVTSRSTASHTLSTRNKED 516  
Db 494 VSHSVTVNVPGRGLALSLS--PRLAPAGASANGHHQDPGYVYKHGSISEN-SLPSSGPE 550  
QY 517 SGRQRDDILM-----EKPSRPMESNPDT 539  
Db 551 PGTKDDGYLNGSLYEPWVGEQPPPLEEERET 583  
RESULT 4  
PTRR\_PIG  
ID PTRR\_PIG STANDARD; PRT; 585 AA.  
AC P50133;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 15-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR  
DE PRECURSOR (PTH/PTHr RECEPTOR).  
GN PTHr1 OR PTHr.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96305358; PubMed=8688470;  
RA Black E.C., Smith D.P., Zhang X.Y., Frolk C.A., Harvey A.,  
RA Chandrasekhar S., Hsiung H.M.;  
RT "Structure and functional expression of a complementary DNA for  
RT porcine parathyroid hormone/parathyroid hormone-related peptide  
RT receptor".;  
RL Blochim. Biophys. Acta 1307:339-347(1996).  
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR  
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS  
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL  
CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER  
CC SYSTEM (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN  
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; U18315; AAC48619.1; -  
CC GCRDb; GCR\_1607; -  
CC InterPro; IPR000832; -  
CC InterPro; IPR002170; -  
CC Pfam; PF00002; 7tm\_2; 1.  
CC PRINTS; PR00249; GPCRSECRETIN.  
CC PRINTS; PR00393; PTHHORMONER.  
CC PROSITE; PS00649; G\_PROTEIN\_RECEPT\_F2\_1; 1.  
CC PROSITE; PS00650; G\_PROTEIN\_RECEPT\_F2\_1; 1.  
CC PROSITE; PS00227; G\_PROTEIN\_RECEPT\_F2\_3; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 26 POTENTIAL.  
FT CHAIN 27 585 PARATHYROID HORMONE/PARATHYROID HORMONE-  
FT RELATED PEPTIDE RECEPTOR.  
FT DOMAIN 27 184 EXTRACELLULAR (POTENTIAL).  
FT

FT TRANSMEM 185 208 1 (POTENTIAL).  
FT DOMAIN 209 215 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 216 235 2 (POTENTIAL).  
FT DOMAIN 236 277 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 278 301 3 (POTENTIAL).  
FT DOMAIN 302 315 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 316 337 4 (POTENTIAL).  
FT DOMAIN 338 356 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 357 377 5 (POTENTIAL).  
FT DOMAIN 378 404 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 405 423 6 (POTENTIAL).  
FT DOMAIN 424 435 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 436 458 7 (POTENTIAL).  
FT DOMAIN 459 585 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 147 147 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 162 162 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 172 172 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 585 AA; 65682 MW; 60BE15CD49B7D210 CRC64;  
Query Match 46.3%; Score 1345; DB 1; Length 585;  
Best Local Similarity 52.5%; Pred. No. 1.2e-96;  
Matches 259; Conservative 75; Mismatches 101; Indels 58; Gaps 7;  
QY 4 LGASLHWGWLMLGSCLL---ARAQLSDSGTITIEQIVLVLKAKYQCELNITAIQLQ--- 57  
Db 1 MGAARTAPGLALLCCPVLSSAVALVDADDVMTKEQIFLLHRAQAQCEKRLKEVLQRP 60  
QY 58 -----BGEN-----CFPEWGLICWPRGTVG 79  
Db 61 DIMESDKWASAPTSKPRKEKASGLYPESGDTGSRHQGRCLPEWHDILCWPLGAPG 120  
QY 80 KISAVPCPPYIYDNHKGVAFRHCNPNGTWDFMHSNLKNTWANSYDCILRFLOPDISIGKQE 139  
Db 121 EVVAMPCCPDYIDFNHKGHAIRCDRNGSWELVPGHNKRWANISECVKLTNETR--ERE 178  
QY 140 FCERLYVMVTGYSISFGSLAVAILIGYFRRLHCHTNTYIHMHLFVSFMLRATSIKVD 199  
Db 179 VFDRLGMIVTVGYSVSLASLTAVAILAYFRRLHCHTNTYIHMHLFVSFMLRAVSIK 238  
QY 200 VVIAHGVVELESIMQD-----DPQNSIEATSDVKQSYQICKIAVWFIYFLATNYW 253  
Db 239 VLYSGATLDEAERLTEELRAIAQAFLPPVAATS-----YVGRVAVTFYFLATNYW 293  
QY 254 ILVEGLYHLNLIFFVAFSDTKYLMGFILGWGPPAFAVAWAVARATLADARCWELSGAD 313  
Db 294 ILVEGLYHLNLIFFVAFSEKKYLMGFVFGWGLPALFVAVWVSVRATLANTGCMWLLSGN 353  
QY 314 IKWYQAPILAAIGLNFILNLTNVRVLATKIWETNAVGHDTKQYRKRLAKSTLVLVLF 373  
Db 354 KKWIIQVILASVLNFIINTVRLATKLRNAGRCDTROQYRKLLKSTLVLMPLFG 413  
QY 374 VHYIVFVCLPHS-FTGLGWEIRMHCELFNSFGFFVYIIYCYCNGEVOAEVKKMWSRN 432  
Db 414 VHYIVFMATPYTESVTLMQVMHYEMLFNSFGFFVYIIYCYCNGEVOAEIKKWSRW 473  
QY 433 LSVDMKRTPECGS 445  
Db 474 LALDFKRRKARSGS 486  
RESULT 5  
PTRR\_HUMAN  
ID PTRR\_HUMAN STANDARD; PRT; 593 AA.  
AC Q03431;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR  
DE PRECURSOR (PTH/PTHr RECEPTOR).  
GN PTHr1 OR PTHr.  
OS Homo sapiens (Human).  
FT

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=93238641; PubMed=8386612;  
RA Schipani E., Karga H., Karaplis A.C., Potts J.T. Jr., Kronenberg H.M.,  
RA Abou-Samra A.-B., Segre G.V., Jueppner H.;  
RT "Identical complementary deoxyribonucleic acids encode a human renal  
RT and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";  
RL Endocrinology 132:2157-2163(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=93387403; PubMed=8397094;  
RA Schneider H., Feyen J.-H., Rao Movva N.;  
RT "Cloning and functional expression of a human parathyroid hormone  
RL receptor.";  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95263723; PubMed=7745008;  
RA Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.F.,  
RA Stuhmann M., Kruse K., Whyte M.P., Murray T., Schmidtke J., Dop C.,  
RA Brickman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M.,  
RA Abou-Samra A.-B., Segre G.V., Jueppner H.;  
RT "Pseudohypoparathyroidism type 1b is not caused by mutations in the  
RT coding exons of the human parathyroid hormone (PTH)/PTH-related  
RT peptide receptor gene.";  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95215874; PubMed=7701349;  
RA Schipani E., Kruse K., Jueppner H.;  
RT "A constitutively active mutant PTH-PTHrP receptor in Jansen-type  
RL metaphyseal chondrodysplasia.";  
RN [5]  
RP VARIANT MURK-JANSEN ARG-223 AND PRO-410.  
RX MEDLINE=96366745; PubMed=8703170;  
RA Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,  
RA Kooh S.W., Cole W.G., Jueppner H.;  
RT "Constitutively activated receptors for parathyroid hormone and  
RT parathyroid hormone-related peptide in Jansen's metaphyseal  
RL chondrodysplasia.";  
RN [6]  
RP VARIANT MURK-JANSEN ARG-223 AND PRO-410.  
RX MEDLINE=96366745; PubMed=8703170;  
RA Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,  
RA Kooh S.W., Cole W.G., Jueppner H.;  
RT "Constitutively activated receptors for parathyroid hormone and  
RT parathyroid hormone-related peptide in Jansen's metaphyseal  
RL chondrodysplasia.";  
RN [7]  
RP VARIANT MURK-JANSEN ARG-223 AND PRO-410.  
RX MEDLINE=96366745; PubMed=8703170;  
RA Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,  
RA Kooh S.W., Cole W.G., Jueppner H.;  
RT "Constitutively activated receptors for parathyroid hormone and  
RT parathyroid hormone-related peptide in Jansen's metaphyseal  
RL chondrodysplasia.";  
RN [8]  
RP MUTAGENESIS OF ARG-223 AND PRO-410.  
RX MEDLINE=97322091; PubMed=9178745;  
RA Schipani E., Jensen G.S., Pincus J., Nissenson R.A., Gardella T.J.,  
RA Juppner H.;  
RT "Constitutive activation of the cyclic adenosine 3',5'-monophosphate  
RT signaling pathway by parathyroid hormone (PTH)/PTH-related peptide  
RT receptors mutated at the two loci for Jansen's metaphyseal  
RL chondrodysplasia.";  
RN [9]  
RP M.O. Endocrinol. 11:851-858(1997).  
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR  
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS  
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL  
CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER

CC SYSTEM.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. MOST ABUNDANT IN  
CC KIDNEY, BONE AND LIVER.  
CC -1- DISEASE: DEFECTS IN PTHRI ARE THE CAUSE OF BLOWSTRAND TYPE OF  
CC CHONDRODYSPLASIA; A SEVERE SKELETAL DYSPLASIA.  
CC -1- DISEASE: DEFECTS IN PTHRI ARE THE CAUSE OF MURK-JANSEN TYPE OF  
CC METAPHYSEAL CHONDRODYSPLASIA; A SEVERE SKELETAL DYSPLASIA. IT IS  
CC A RARE FORM OF SHORT-LIMBED DWARFISM ASSOCIATED WITH HYPERCALCEMIA  
CC AND NORMAL OR LOW SERUM CONCENTRATIONS OF THE TWO PARATHYROID  
CC HORMONES.  
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC  
CC EMBL; L04308; AAA36525.1; -  
CC EMBL; X68596; CAA48389.1; -  
CC EMBL; U22409; AAB60657.1; -  
CC EMBL; U22401; AAB60657.1; JOINED.  
CC EMBL; U22402; AAB60657.1; JOINED.  
CC EMBL; U22403; AAB60657.1; JOINED.  
CC EMBL; U22404; AAB60657.1; JOINED.  
CC EMBL; U22405; AAB60657.1; JOINED.  
CC EMBL; U22406; AAB60657.1; JOINED.  
CC EMBL; U22407; AAB60657.1; JOINED.  
CC EMBL; U22408; AAB60657.1; JOINED.  
CC EMBL; U17418; AAA56774.1; -  
CC PIR; S29610; S29610.  
CC PIR; A49191; A49191.  
CC PDB; 1BL1; 30-MAR-99.  
CC GCRDb; GCR\_0205; -  
CC GCRDb; GCR\_0647; -  
CC GCRDb; GCR\_1335; -  
CC GCRDb; GCR\_2025; -  
CC MIM; 168468; -  
CC MIM; 156400; -  
CC MIM; 215045; -  
CC InterPro; IPR000832; -  
CC InterPro; IPR002170; -  
CC Pfam; PF00002; 7tm\_2; 1.  
CC PRINTS; PR00249; GPCRSECRETIN.  
CC PROSITE; PS00393; PTRHORMONER.  
CC PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
CC PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
CC PROSITE; PS00227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
KW Disease mutation; 3D-structure.  
FT SIGNAL 1 26  
FT CHAIN 27 593  
FT DOMAIN 27 188  
FT TRANSMEM 189 212  
FT DOMAIN 213 219  
FT TRANSMEM 220 239  
FT DOMAIN 240 282  
FT TRANSMEM 283 306  
FT DOMAIN 307 320  
FT TRANSMEM 321 342  
FT DOMAIN 343 361  
FT TRANSMEM 362 382  
FT DOMAIN 383 409  
FT TRANSMEM 410 428  
FT DOMAIN 429 440  
FT TRANSMEM 441 463  
FT DOMAIN 464 593  
FT CARBOHYD 151 151  
FT CARBOHYD 161 161

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FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 H -> R (IN MURK JANSEN; CONSTITUTIVELY
FT VARIANT 223 223 ACTIVATED).
FT FT
FT FT
FT VARIANT 410 410 T -> P (IN MURK JANSEN; CONSTITUTIVELY
FT FT ACTIVATED).
FT FT
FT CONFLICT 471 471 K -> N (IN REF. 2).
FT CONFLICT 473 473 S -> C (IN REF. 2).
FT FT
SQ SEQUENCE 593 AA; 66360 MW; DA1400640A6C7F2B CRC64;

Query Match 46.0%; Score 1336.5; DB 1; Length 593;
Best Local Similarity 47.4%; Pred. No. 5.4e-96;
Matches 276; Conservative 81; Mismatches 134; Indels 91; Gaps 11;

QY 22 ARAQLDSGTITTEEIVLVKAKVOCELNITAQLQ-----CFPEWDGLICPRGTGKISAVPCPPYIYDFNHK 96
Db 22 AYALVDADDVMTKEQIFLHRAQAQCEKRLKEVLQRPASIMESDKGWTSASTSGKPRKD 81

QY 58 -----EGEGN-----CFPEWDGLICPRGTGKISAVPCPPYIYDFNHK 96
Db 82 KASKGLYPESEEDKEAPTSRGYRCLEPDWDHILCPGAGEVAVPCPDYIYDFNHK 141

QY 97 GVAFRHCNPNGTWDFHSLNKTWANSYDCLRFLOPDISIGKQECERLYVMYTVGVYSISF 156
Db 142 GHAYRCRDRNGSWELVPGHNRWTWANSYDCLRFLOPDISIGKQECERLYVMYTVGVYSISF 199

QY 157 GSLAVAILIGYFRLHCTRNTHMLHLSFVSMRLRATSIFFKDRVVAHIGVKELES--- 213
Db 200 ASLTAVAILAYFRLHCTRNTHMLHLSFVSMRLRATSIFFKDRVVAHIGVKELES--- 259

QY 214 -----IMQDDPONSIEATSDVKSOYIGCKTAVVMFYFLATNYWILVEGLYLNHLIFVAF 269
Db 260 ELRAIAQAPPPATAAG-----YACRVAVTFELFLATNYWILVEGLYLNHLIFMAF 314

QY 270 FSDTKLWGLFILGWGPPAAFAVAAVARATLADARCWELSGADIKWYQAPILAAIGLN 329
Db 315 FSEKYLWGLTFVGLPGLVAVFVAVSVRATLANTGCDWLDSSGNKWIIVQVPLASIVLN 374

QY 330 FILFLATVRLATKIETHNAVGHDTKQYRKLAKSTLVLVLEGVHYIVFVCLPHS-FIG 388
Db 375 FILFLATVRLATKIETHNAVGHDTKQYRKLAKSTLVLVLEGVHYIVFVCLPHS-FIG 434

QY 389 LGWEIRHCHLFFNSFGFVSIYCYNGEVAQAEVKMWSNLSVDWKRTPPCGSRRRC 448
Db 435 TLWQVQMHYEMLFNSFGFVSIYCYNGEVAQAEVKMWSNLSVDWKRTPPCGSRRRC 494

QY 449 G-SVLTVTHTSSQSQVAAAHAWCLSLAKLPRSPADSLTATSL-YLWSGVGTQST-AS 505
Db 495 SYGPMVSHTSVTNVPGRVGLG-----LPLSPRLPTATTNGHPQLPGHAKPGTAL 545

QY 506 HTLSTRS-----NKEDSGRQRDDILMEK 528
Db 546 ETLETPPAMAAPKDDGFLNGSCGLDEASGPERPALLQE 587

RESULT 6
PTRR_RAT
ID PTRR_RAT STANDARD; PRT; 591 AA.
AC P25961;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
DE PRECURSOR (PTH/PTHrP RECEPTOR).
GN PTHrP OR PTHr.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
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RP SEQUENCE FROM N.A.
RC TISSUE=Bone;
RX MEDLINE=92212903; PubMed=1313566;
RA Abou-Samra A.-B., Jueppner H., Force T., Freeman M.W., Kong X.-F.,
RA Schipani E., Urena P., Richards J., Bonventre J.V., Potts J.T. Jr.,
RA Kronenberg H.M., Segre G.V.;
RT "Expression cloning of a common receptor for parathyroid hormone and
RT parathyroid hormone-related peptide from rat osteoblast-like cells: a
RT single receptor stimulates intracellular accumulation of both cAMP
RT and inositol triphosphates and increases intracellular free
RT calcium."
RT Proc. Natl. Acad. Sci. U.S.A. 89:2732-2736(1992).
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=94292182; PubMed=8020952;
RA Pausova Z., Bourdon J., Clayton D., Mattel M.-G., Seldin M.F.,
RA Janicik N., Riviere M., Szpirer J., Levay G., Szpirer C.;
RT "Cloning of a parathyroid hormone/parathyroid hormone-related peptide
RT receptor (PTHrP) cDNA from a rat osteosarcoma (UMR 106) cell line:
RT chromosomal assignment of the gene in the human, mouse, and rat
RT genomes."
RL Genomics 20:20-26(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC SYSTEM.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

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EMBL; M77184; AAA41811.1; -;
DR EMBL; L19475; AAA68098.1; -;
DR GCRDb; GCR_0206; -;
DR GCRDb; GCR_0938; -;
DR InterPro; IPR000832; -;
DR InterPro; IPR002170; -;
DR Pfam; PF00002; 7tm2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRINTS; PR00393; PTHRMONER.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_4; 1.
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DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_6; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_7; 1.
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DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_42; 1.
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DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_45; 1.
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DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_47; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_48; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_49; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_50; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_51; 1.
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FT TRANSMEM 370 392 7 (POTENTIAL).
FT DOMAIN 393 440 7 (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 124 124 G -> A (IN REF. 1).
FT CONFLICT 210 210 A -> P (IN REF. 2).
FT CONFLICT 308 308 I -> F (IN REF. 3).
FT CONFLICT 333 333 E -> Q (IN REF. 3).
FT CONFLICT 377 377 G -> A (IN REF. 1).
SQ SEQUENCE 440 AA; 50206 MW; E22CDD0EE7C0ACCI CRC64;

Query Match 27.0%; Score 784; DB 1; Length 440;
Best Local Similarity 38.4%; Pred. No. 1.9e-53;
Matches 178; Conservative 64; Mismatches 138; Indels 84; Gaps 14;

Qy 13 WMLGSL--LARAQSDSGTITTEEQIVLVKAKVQCELNITAOQEGNCFPEWGL 70
Db 39 WEEQDQCLQELSREQTGLGT-----EQPV-----PCCEGMWDNI 73

Qy 71 ICWPRGTGKISAVPCPPYIDF-NHKGVAFRHCNPGTDFMHSLNKTNWYSDCLRFL 129
Db 74 SCWSSVPCRWVECPFLMLTSRNSGLFRNCTQDG-----WSE-----TFP 117

Qy 130 QPDISG-----KQECERLYVMYTVGYISFGSLAVAILIIGYFRRLHCTRNYI 179
Db 118 RPNLACGVNVDSSNEKRHSYLLKLVMTYGVSSSLVALLVALGILCAFRRLHCTRNYI 177

Qy 180 HMLFVSPMLRATSFVDRVVAHIGVKELESIMQDDPQNSIATSVDSKSYQIGCKIA 239
Db 178 HMLFVSPILRALSFIKDAV-----LFSSDD-----VTYCD-AHRAGCKLV 218

Qy 240 VMFTYFLATNYWTLVGLVHLNLFVAFSTDYKYLWGLFGLGFPAAFAVAWAVARA 299
Db 219 MVLQYCYTMANYSWLLVGLVHLTLTLLATSFSEYKYLQGVAFWGSFAIFVALWAIARH 278

Qy 300 TLADARCWELSA-GDIKWIYQAPILAAIAGLNFLFNTVRLVATKIWETNAVGHDTKQY 358
Db 279 FLEDVGCMDINANASIMWIIRGPVLSILINFLINILRILMRKLRTQETRGNEV-SHY 337

Qy 359 RKLAKSTLVLVFVGVHVVVFCPLPHSTFTGLGWETRMHCELFNFSQGFVSIYCYCNG 418
Db 338 KRLARSTLLPLFGIHYIVFAFSPED-----AMEIQLFELALGSGFGLVAVLYCFLNG 393

Qy 419 EVQABVKWNRWNLVDMKTPPCGSRRCGSLVLTFTVTHSTSSQ 462
Db 394 EVQLEVKKKQWQHL-----REFPLHPVASFNSNTKASHLEQSQ 432

RESULT 12
VIPR_CARAU STANDARD; PRT; 447 AA.
AC Q90308;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR (VIP-R) (VIP RECEPTOR).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
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CC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190233; PubMed=9038250;
RA Chow B.K.C., Yuen T.T.H., Chan K.W.;
RT "Molecular evolution of vertebrate VIP receptors and functional
characterization of a VIP receptor from goldfish Carassius auratus.";
RL Gen. Comp. Endocrinol. 105:176-185(1997).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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or send an email to license@isb-sib.ch).
CC EMBL; U56391; AAB05459.1; -.
DR GCRDB; GCR_1205; -.
DR InterPro; IPR000832; -.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G-PROTEIN_REC_F2_1; 1.
DR PROSITE; PS00650; G-PROTEIN_REC_F2_2; 1.
DR PROSITE; PS00627; G-PROTEIN_REC_F2_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 103 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 104 128 1 (POTENTIAL).
FT DOMAIN 129 135 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 136 155 2 (POTENTIAL).
FT DOMAIN 156 178 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 179 202 3 (POTENTIAL).
FT DOMAIN 203 216 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 217 238 4 (POTENTIAL).
FT DOMAIN 239 255 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 257 280 5 (POTENTIAL).
FT DOMAIN 281 305 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 306 325 6 (POTENTIAL).
FT DOMAIN 326 337 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 338 357 7 (POTENTIAL).
FT DOMAIN 358 447 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 447 AA; 50959 MW; 66839E243702554C CRC64;

Query Match 26.9%; Score 782; DB 1; Length 447;
Best Local Similarity 35.0%; Pred. No. 2.8e-53;
Matches 165; Conservative 82; Mismatches 137; Indels 88; Gaps 12;

Qy 44 AKVQCELNITAOQEGNCFPEWGLICWPRGTGKISAVPCPPYIDF--NHKGVAFR 101
Db 11 ARARCNKTAGNVTSG---CKGMWDIIACWPSAKVGEHVIVPCPNYFRHFSDHGNSLSK 67

Qy 102 HCNPNGTWDFM-----HSLNKTWANYSDCLRFLQPDISICKQECERLYWYTVG 151
Db 68 TCTADG-WTEMDPMETIAVYCGYNLNGT-----VDDSFRRSVKIGTYIG 110

Qy 152 YSISFGSLAVAILIIGYFRRLHCTRNYIHMHLFVFMRLRATSFVDRVVAHIGVKELE 211
Db 111 HVSLSLSLTAVILCMRSKRLHCTRNYIHMHLFVFSILKAIKIAVFKDAVLY----- 161

Qy 212 SLIMQDDPQNSIATSVDSKSYQIGCKIAVVMFYFLATNYWTLVGLVHLNLFVAFVS 271
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Db 162 DVIOESD--NCSTAS-----VGKAVIVFQYCIIMASFFWLLVEGLYLHALLAVSFFS 212
QY 272 DTKYLMGFLIGWGPFAAFAVAARATLADARWEL--SAGDIKWIIQAPILAAIGLN 329
Db 213 ERKYFWYILIGWGPFIIMASFAKAYFNDVGCWDIENSDFWIIKTIPLASILMN 272
QY 330 FILFLNTVRVLTATKIWETNAVGHDTKQYKRLAKSTPLVLVLVFGVHYIVFVCLPHSFTGL 389
Db 273 FILFICIIIRLRQKI-NCPDIGNESNQYSRLAKSTPLLLPLFGINFIIFAFIPEN--I 328
QY 390 GWEIRHMCLEFNSFGFFVSIYCYCNGEVOAEVKKMSRWNL----- 433
Db 329 KYELRLVFDLILGSGFGFVAVLYFLNGEVOAEIKRWRHLEFLGPDTKYQHPSMG 388
QY 434 -----SVDKKTTPCGSRRCGSLVLTVTTHSTSSOSQVAAAH 469
Db 389 SNGNFEISTOISMLTRCSPTFRASQCDETSITVLGSLTMGYCHQNETVKGH 440

RESULT 13
VIPR_RAT
ID VIPR_RAT STANDARD; PRT; 459 AA.
AC P30083;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1)
DE (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR)
DE (PACAP TYPE II RECEPTOR) (PACAP-R-2).
GN VIPRL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=92232309; PubMed=1314625;
RA Ishihara T., Shigemoto R., Mori K., Takahashi K., Nagata S.;
RT "Functional expression and tissue distribution of a novel receptor
RT for vasoactive intestinal polypeptide.";
RL Neuron 8:811-819(1992).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: IN LIVER, LUNG, INTESTINES, THYMUS AND BRAIN
CC (MOSTLY IN THE CEREBRAL CORTEX AND HIPPOCAMPUS).
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
CC EMBL: M86835; AAA42331.1; -.
CC PIR: JH0594; JH0594.
CC GCRdb; GCR_0369; -.
CC InterPro; IPR000832; -.
CC InterPro; IPR001571; -.
CC InterPro; IPR001771; -.
CC Pfam; PF00002; 7tm.2; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC PRINTS; PR00491; VASOACTIVEIPR.
CC PRINTS; PRO1154; VIPRECEPTOR.
CC PROSITE; PS00649; G-PROTEIN_RECEP_F2.1; 1.
CC PROSITE; PS00650; G-PROTEIN_RECEP_F2.2; 1.
CC PROSITE; PS02227; G-PROTEIN_RECEP_F2.3; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
CC SIGNAL
CC 1 30
CC POTENTIAL.
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FT CHAIN 31 459 VASOACTIVE INTESTINAL POLYPEPTIDE
FT DOMAIN 31 143 RECEPTOR 1.
FT TRANSMEM 144 168 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 169 175 1 (POTENTIAL).
FT TRANSMEM 176 195 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 196 217 2 (POTENTIAL).
FT TRANSMEM 218 241 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 242 255 3 (POTENTIAL).
FT TRANSMEM 256 277 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 278 294 4 (POTENTIAL).
FT TRANSMEM 295 318 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 319 343 5 (POTENTIAL).
FT TRANSMEM 344 363 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 364 375 6 (POTENTIAL).
FT TRANSMEM 376 395 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 396 459 7 (POTENTIAL).
FT CARBOHYD 58 459 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 59 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 69 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 100 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 292 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 459 AA; 52057 MW; 99E8957DA86698D2 CRC64;

Query Match 26.6%; Score 772.5; DB 1; Length 459;
Best Local Similarity 36.8%; Pred. No. 1.5e-52;
Matches 172; Conservative 78; Mismatches 134; Indels 83; Gaps 17;

QY 36 EQIVLVKAKVOCELNITAAQLEGEGNCPPEWDGLICPRGIVGKISAVPCP-----PY 89
Db 38 EYLQIETIQROQCLEE--AQLENETTGCSKMDNLTCWPTTPRGOAVLDCPLIFQLFAP 95
QY 90 IYDFNHKGVAFRHCPNGTWDPMHSLINKTWANYSCLRFLOP---DISIG----- 136
Db 96 INGYN-----ISRSCTEEG-----WSQ-----LECPYHACGLNDRASSLDE 133
QY 137 --KQEFCELYVMYTVGYISFSGSLAVAILIIGYFRRHLHCTRNYTHMHLFVSFMLRATSI 194
Db 134 QOQTKFRVTKVTGYTIGYSLASLAVAMAILSLFRKLHCTRNYTHMHLFMSFILRATAV 193
QY 195 FVKDRVVAHIGVKESLIMODDPQNSTEATSVDKSOYIGCKIAVVMFIYLAIFYWI 254
Db 194 FIKDMALF-----NSGEIDHCSEAS--VGCKAAVVFQYCYMANFFWL 234
QY 255 LVEGLYLHNLIEVAFPSDTKYLWGFLLIGWFPFAAFVAARATLADARWEL--LSAGD 313
Db 235 LVEGLYLYLLAVSFESERKEYEWGILIGWGPSVFIITWTVVRIYFDFGCDWTIINS 294
QY 314 IKWIYOAPILAAIGLNFILFLNTVRVLTATKIWETNAVGHDTKQYKRLAKSTPLVLVLVFG 373
Db 295 LWWIIKAPILLILVNFVLFICIRILVQKLRPPD--IGKNDSSPYSRLAKSTLLLLPLFG 353
QY 374 VHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGFFVSIYCYCNGEVOAEVKKMSRWNL 433
Db 354 IHVYVMAFFPDNFKA---QVKMVFELVWGSGFGFVAVLYFLNGEVOAEIKRWRHNL 410
QY 434 S--VDM--KRTPPCGSRR---CG---SVLTVT---HSTSSQSOVA 466
Db 411 QGVIGNSKSKSQHPWGSNGCATCTQVSMLTRVSPSARRSSSFQAEVS 457

RESULT 14
VIPR_HUMAN
ID VIPR_HUMAN STANDARD; PRT; 457 AA.
AC P32241; Q15871;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1)
DE (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR)
DE (PACAP TYPE II RECEPTOR) (PACAP-R-2).
GN VIPRL.
OS Homo sapiens (Human).
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RESULT 15  
VIPS\_MOUSE  
ID VIPS\_MOUSE STANDARD; PRT; 437 AA.  
AC P41588; P97750;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE VASOACTIVE INTENSINAL POLYPEPTIDE RECEPTOR 2  
DE (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE III RECEPTOR)  
DE (PACAP TYPE III RECEPTOR) (PACAP-R-3).  
GN VIPR2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6;  
RX MEDLINE=94195806; PubMed=81461174;  
RA Inagaki N., Yoshida H., Mizuta M., Mizuno N., Fujii Y., Gonoi T.,  
RA Miyazaki J.-I., Seino S.;  
RT "Cloning and functional characterization of a third pituitary  
RT adenylate cyclase-activating polypeptide receptor subtype expressed  
RT in insulin-secreting cells.";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:2679-2683(1994).  
RN [2]  
RP SEQUENCE OF 149-407 FROM N.A.  
RC STRAIN=BALB/C; TISSUE=Thymus;  
RX MEDLINE=96378694; PubMed=8784257;  
RA Delgado M., Martinez C., Johnson M.C., Gomariz R.P., Ganea D.;  
RT "Differential expression of vasoactive intestinal peptide receptors 1  
RT and 2 (VIP-R1 and VIP-R2) mRNA in murine lymphocytes.";  
RL J. Neuroimmunol. 68:27-38(1996).  
CC -1- FUNCTION: THIS IS A RECEPTOR FOR VIP AS WELL AS PACAP-38 AND -27,  
CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH  
CC ACTIVATE ADENYL CYCLASE. CAN BE COUPLED TO PHOSPHOLIPASE C.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE MIN6 CELLS,  
CC AT MODERATE LEVELS IN PANCREATIC ISLETS, INSULIN-SECRETING CELLS,  
CC LUNG, BRAIN, STOMACH, AND COLON, AND AT LOW LEVELS IN THE HEART.  
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
CC -----  
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CC -----  
DR EMBL; D28132; BAA05674.1; -;  
DR EMBL; S82966; -; NOT\_ANNOTATED\_CDS.  
DR GCRDB; GCR\_1028; -;  
DR GCRDB; GCR\_1856; -;  
DR MGD; MGI:107166; Vipr2.  
DR InterPro; IPR000832; -;  
DR InterPro; IPR001571; -;  
DR InterPro; IPR002284; -;  
DR Pfam; PF00002; 7tm.2; 1.  
DR PRINTS; PR00249; GPCRSECRETIN.  
DR PRINTS; PR00491; VASOACTIVEIPR.  
DR PRINTS; PR01155; VIP2RECEPTOR.  
DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_3; 1.  
DR PROSITE; PS50227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 437 VASOACTIVE INTESTINAL POLYPEPTIDE  
FT RECEPTOR 2.  
FT DOMAIN 23 125 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 126 150 1 (POTENTIAL).  
FT DOMAIN 151 157 CYTOPLASMIC (POTENTIAL).  
FT

FT	TRANSMEM	158	177	2 (POTENTIAL).
FT	DOMAIN	178	202	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	203	226	3 (POTENTIAL).
FT	DOMAIN	227	239	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	240	261	4 (POTENTIAL).
FT	DOMAIN	262	278	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	279	302	5 (POTENTIAL).
FT	DOMAIN	303	327	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	328	347	6 (POTENTIAL).
FT	DOMAIN	348	359	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	360	379	7 (POTENTIAL).
FT	DOMAIN	380	437	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	57	57	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	91	91	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	357	357	A -> P (IN REF. 2).
SQ	SEQUENCE	437 AA: 49473 MW: CCC870A094F9DC90 CRC64;		

Query Match 24.5%; Score 713.5; DB 1; Length 437;  
Best Local Similarity 33.6%; Pred. No. 5.3e-48;  
Matches 163; Conservative 87; Mismatches 156; Indels 79; Gaps 15;

QY	39	VLVLKAKVOCELNITAOLOEGEGNCPP-----	-----EWDGLICWPRGTVGKISAV	84	
DB	13	LLVRVSSIHPECRFHLEIQEETKCAELLSQTE	NORACSGVMDNITCWPRADVGTVTV	72	
QY	85	PCPPYIYDF-NHKGVAFRHCNPNGTWDFMHS	LNKTWANSDDLRLFLQDISIGKQEFCE	143	
DB	73	PCPKVFSNYSRPGNISKNCTSDG-W-----	SETPPFDIACGYNDPE-DESKISFYIL	124	
QY	144	LYVMYVGYSGISFGSLAVAILIGYFRRRLHC	TRNYIHMLFVSFMLRATSIFVKDRVHA	203	
DB	125	VRAIYTLGYSVLSMLSTTGSIIICLFRLHC	TRNYIHLNLFSLRALSVLVKDSVLVS	184	
QY	204	HIGVKELESILWDDPQNSIEATSDVKSIYCK	IAVVMFTYPLATNYWILVEGLYLHN	263	
DB	185	SSGL-----LRCHDQP-----	ASWVGCKLSLVFFQYICIMANFYWLLVE	228	
QY	264	LIFVAFESDTKYLWGLFILIGWGFPAFVA	AAVARATLADARCWELSGADIK-WIYO	322	
DB	229	LL-VAILPSRCFLAYLLLGWGPSCVIGAW	TATRLSLEDTCGWDNDNHSIPWVIRMPI	287	
QY	323	LAAILNFIILNTVRVLATKIWETNAVGH	TRKQYKRLAKSTLVLVLVFGVHYIVFVCL	382	
DB	288	LISIVVNFALFISIVRILKQLTSPDVGND	-QSQYKRLAKSTLLIPLFGVHYMVFAAF	346	
QY	383	PHSFTGLGWEIRMHCELPNSFGQFVSII	YCYCNGCEVOAEVKKMSRNLSVDWKR	442	
DB	347	P---IGISSTYQILFELCVGSGFGLVAV	LYCYFLNSEVOCELKRRWR-----	390	
QY	443	CGSRRCGSLVTTVTHSTSSQSOVAAAHA	ACLSLAKLPSPADSLTATSLYLAMSGVTQ	502	
DB	391	-----GLCL-----	TQAGSRDYRLHSHSMS-----RNGSES	-----ALQIHRGSRQTQSF	429
QY	503	TASHT 507			
DB	430	LOSET 434			

Search completed: September 21, 2001, 17:08:50  
Job time: 183 sec







Result No.	Query		Length	DB	ID	Description
	Score	Match				
1	1677.5	57.7	575	13	Q9PW87	Q9pw87 brachydonic
2	1418.5	48.8	536	13	Q9PVD3	Q9pvd3 brachydonic
3	1345.5	46.3	595	6	Q9TU31	Q9tu31 canis famill
4	1307.5	45.0	542	13	Q9PVD2	Q9pvd2 brachydonic
5	858.5	29.5	169	11	Q9RLD4	Q9rld4 mus musculu
6	814	28.0	444	13	Q9YH6C	Q9yh6c rana ridibun
7	791.5	27.2	459	11	Q9RI18	Q9rl18 mus musculu
8	791.5	27.2	459	11	Q9JI40	Q9ji40 mus musculu
9	780.5	26.8	418	13	Q9IB23	Q9ib23 gallus gallu
10	713	24.5	465	13	Q73789	Q73789 carassius a
11	702.5	24.2	438	13	Q73768	Q73768 carassius a
12	685.5	23.6	465	13	Q9PTK1	Q9ptk1 xenopus lae
13	636	21.9	423	6	Q9N1F8	Q9n1f8 bos taurus
14	633	21.8	441	6	Q9TUJ0	Q9tujo bos taurus
15	610	21.0	404	6	Q9TUJ1	Q9tuji bos taurus
16	604	20.8	439	11	Q9WU99	Q9wu99 rattus norv
17	592	20.4	492	13	Q9PUK1	Q9puki hoplobatrach
18	566.5	19.5	589	6	Q9GMD1	Q9gmd1 oryctolagus
19	554	19.1	359	4	Q9HB45	Q9hb45 homo sapien

QY	85	PCPGYIYDFNHKGAVFRHONPNGTWDFMHSLNKTNWYSDCLRFQPDISIGKQECERL	144
Db	115	PCPGYIYDFNHAHARRCDNSGSSVLAESSNKTWVNYTECIK--SPENKKRQVFPERL	172
QY	145	YVMYTVGYSISGSLAVAILIIGYFRRLHCTRNYIMHILFVSEMLRATSIYVKDRVVHAH	204
Db	173	HIMYTVGYAVSFSSLLVAIFIIGYFRRLHCTRNYIMHILFVSEMLRAAASIFVKDRHVYHTS	232
QY	205	IGVKELESIMODDPONSTEATSVDKSOYIGCKIAVMMYIYFATNYWYLVEGLYHLNL	264
Db	233	AGLQESDAVLM--NNFTNAVDPVDTOSYMGCKVTVLLFIYFATNYWYLVEGLYHLNL	291
QY	265	IFVAFSDTKYLMGFTLIGWGPFAAFAAWAVARATLADARCWELSGADIKWIYQAPILA	324
Db	292	IFMAFLSDSKYLMGFTLIGWGPFAVFAAWAVVRATLADARCWELSGAGNIKWYQVPILT	351
QY	325	AIGLNFILFNTVRVLTATKIETNAVGHDRKQYRKLAKSTLVLVLFVGVHYHIVFVCLPH	384
Db	352	AIGLNFILFNVIVRVLTAKIRETNAGRYDTRKQYRKLAKSTQVLVFPVGVHYHIVFGMPH	411
QY	385	SFTGLGWEIRMHCELFNSFQGFVFIYCYCNGEVOAEVKMWSRWNLSDWKRTPPCG	444
Db	412	TFBGLGWEIRMYCELFNSFQGFVFIYCYCNGEVOETIKKTWTWNLAFDKNKGPVCG	471
QY	445	SRRCGSVLTVTHSTSSQSOVAAAHAMCLSLAKLPRSPADSTATSLYLAMSGVTSRTA	504
Db	472	SNRYGSVLTLGLNNSTSSQOLAAG-----PQTRSTTLFSSRVYRSSGPTVSTHA	522
QY	505	S-----HTLSTRSNK-----EDSGRQDDILMEK--PSRWPNESNPDTE	540
Db	523	TLPGYVLNSDADSLPPSIPEEPEDSAKQVDDILLKESLTPRPSSGLEDDDE	572
RESULT 2			
Q9PVD3	AC	Q9PVD3; PRELIMINARY; PRT; 536 AA.	
DT	01-MAY-2000	(TRENBLrel. 13, Created)	
DT	01-MAY-2000	(TRENBLrel. 13, Last sequence update)	
DT	01-MAR-2001	(TRENBLrel. 16, Last annotation update)	
DE	PARATHYROID HORMONE RECEPTOR PTH1R		
OS	Brachydanio rerio (Zebrafish) (Zebra danio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;		
OC	Cypriniformes; Cyprinidae; Rasbora; Danio.		
ON	NCBI_TaxID=7955;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99428481; PubMed=10497171;		
RA	Rubin D.A., Jueppner H.;		
RT	"Zebrafish Express the Common Parathyroid Hormone/Parathyroid Hormone-		
RT	related Peptide Receptor (PTH1R) and a Novel Receptor (PTH3R) That Is		
RT	Preferentially Activated by Mammalian and Fuguish Parathyroid		
RT	Hormone-related Peptide";		
RL	J. Biol. Chem. 274:28185-28190(1999).		
DR	EMBL; AF132084; AAF01265.1; -.		
DR	HSSP; Q03431; 1BL1.		
DR	InterPro; IPR000832; -.		
DR	Pfam; PF00002; 7tm2.1.		
DR	PRINTS; PR00249; GPCRSECRETIN.		
DR	PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.		
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.		
DR	SMART; SM00008; HormR; 1.		
KW	Receptor.		
SQ	SEQUENCE	536 AA; 61454 MW; 653B0A56DB2C8FA9 CRC64;	
Query Match			
Best Local Similarity			
Matches 269; Conservative 80; Mismatches 107; Indels 9; Gaps 6;			

QY	4	LGASLHV--WGWMIGSCL--LARAOLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEE	60
Db	1	MGATLIVRTLGLFGLTLLSFYGLVDADDVLTKEEQIVLVFNKRAKCKCERAIKSKHKTSE	60
QY	61	GNCFFEWDLICWPRGTGCKISAVPCPPYIDFNHKGAVFRHONPNGTWDFMHSLNKTHA	120
Db	61	GSLCPEDWDGILCWPEGVPGKVMYSTSCPEYIYDFNHKGHAYRCDLNGTWELASHNNKTWA	120
QY	121	NYSDCLRFQPDISIGKQECERLRYVMYTVGYSISGSLAVAILIIGYFRRLHCTRNYIH	180
Db	121	NYSECAKFPFHYNQOREVDFRLIYTVGYSISGSLAVATVILGYFRRLHCTRNYIH	180
QY	181	MHLFVSFMLRATSIYVKDRVHAHIGVKELESIMODDPONSTEATSVDKSOYIGCKIAV	240
Db	181	MHLFVSFMLRAISIFVKDVLVYSGSALQEMERITV--EDLKSITEAPPANKTQFIGCKVAV	239
QY	241	VNFYIFLATNYWYLVEGLYHLNLIFVAFSDTKYLMGFTLIGWGPFAAFAAWAVARAT	300
Db	240	TUFLYIFLATNYWYLVEGLYHLNLIFMTFFSDRKYLMGFTLIGWGPVAMFVTINASVRAT	299
QY	301	LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLTAKIETNAVGHDRKQYR	360
Db	300	LADTECDWLSAGNLKWIYQIPILTAIVNFFLFLNIRVLTAKIETNAGRCDTROQYR	359
QY	361	LAKSTLVLVLFVGVHYHIVFVCLPHS--FTGLGWEIRMHCELFNSFQGFVSIYCYCNGE	419
Db	360	LLKSTLVLMPLFGVHYIVFMAMPYTEVSGVLWQIQMHVEMLENSVQGFVSIYCYCNGE	419
QY	420	VOAEVKMWSRWNLSDWKRTPPCGSR--RCGSVL--TTVTHSTS	460
Db	420	VOAEIKKAWNRRTLALDFKRAKRSNTSYSGPMVSHTSVTNVT	464
RESULT 3			
Q9TU31	AC	Q9TU31; PRELIMINARY; PRT; 595 AA.	
DT	01-MAY-2000	(TRENBLrel. 13, Created)	
DT	01-MAY-2000	(TRENBLrel. 13, Last sequence update)	
DT	01-MAR-2001	(TRENBLrel. 16, Last annotation update)	
DE	PARATHYROID HORMONE RECEPTOR-1.		
GN	PTH1.		
OS	Canis familiaris (Dog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
ON	NCBI_TaxID=9615;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=KIDNEY;		
RA	Smock S.L., Vogt G.A., Castleberry T.A., Lu B., Owen T.A.;		
RT	"Molecular cloning and functional characterization of the canine		
RT	parathyroid hormone receptor-1 (PTH1).";		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF167095; AAD55938.1; -.		
DR	HSSP; Q03431; 1BL1.		
DR	InterPro; IPR000832; -.		
DR	Pfam; PF00002; 7tm2.1.		
DR	PRINTS; PR00249; GPCRSECRETIN.		
DR	PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.		
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.		
DR	SMART; SM00008; HormR; 1.		
KW	Receptor.		
SQ	SEQUENCE	595 AA; 66308 MW; 09568ECF38D4D258 CRC64;	
Query Match			
Best Local Similarity			
Matches 281; Conservative 90; Mismatches 154; Indels 79; Gaps 11;			

Query Match 48.8%; Score 1418.5; DB 13; Length 536;  
Best Local Similarity 57.8%; Pred. No. 5.3e-110;  
Matches 269; Conservative 80; Mismatches 107; Indels 9; Gaps 6;

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QY 58 -----EGEGN-----CFPEWDGLICWPR 75
Db 61 DIMESDKGASASTSGPKKKEKASGLKYPSEEDKEVPGSRHRGRPCLPWDHILCWPL 120
QY 76 GTVGKISAVPCPPYIYDFNHNKGVAFRHNCPNGTWFDMISLNTKNTWANSOCLRFLOPDISI 135
Db 121 GAGGEVAVPCPDYIYDFNHNKGVAFRHNCPNGTWFDMISLNTKNTWANSOCLRFLOPDISI 179
QY 136 KQOECERLYVMYTVGYSTISFGSLAVAILIIGYFRRLHCTRNVIHMLFVSPMLRATSF 195
Db 180 -EREVDFRLGMIYTVGYSVLSLASLTAVALLIAYFRRLHCTRNVIHMLFVSPMLRATSF 238
QY 196 VKDRVYVHAHIGVKELESLESLIMODDPONSIEATSVDKSQYIGCKIAYVMFYFLATNYWIL 248
Db 239 VKDAVLYSGATLDEAERLTEELRAIAQAPPPPTAAA-----GYAGCRVAVTFPLYLELA 292
QY 249 TNYWILVEGLYLHNLIFVAFSFDTKYLMGFTLIGWGPFAAFVAAWAVARATLADARQWE 308
Db 293 TNYWILVEGLYLHNLIFVAFSFDTKYLMGFTLIGWGPFAAFVAAWAVARATLADARQWE 352
QY 309 LSAGDIKWIYQAPILAAIAGLNFILNTVRVLATKIWETNAVGHDTKQYRKLAKSTLVL 368
Db 353 LSSGNKKWIIQVPIIASIVLNFILNTVRVLATKIWETNAVGHDTKQYRKLAKSTLVL 412
QY 369 VLVFGVHYIVFVCLPHS-FTGLGWEIRHCELFNSFGQFFVSIYCYCNGEVAQAEVKRM 427
Db 413 MPLFGVHYIVFVCLPHS-FTGLGWEIRHCELFNSFGQFFVSIYCYCNGEVAQAEVKRM 472
QY 428 WSRNWLSDVWKRTPPCGSRRCGSVLTTHSTSSOSQVAAAHAWCLSLAKLPRSPADSUT 487
Db 473 WSRNWLSDVWKRTPPCGSRRCGSVLTTHSTSSOSQVAAAHAWCLSLAKLPRSPADSUT 531
QY 488 ATSLYLAGSVTQSRASHTL-----STRNKED-----SGRQDDILMEKPSRPMES 535
Db 532 TNGHPPPIGHT--KPGAPTLPATPPATAAPKDDGLNGSCSGLDEEASAPERPPALLQE 589
QY 536 NPDT 539
Db 590 EWET 593

RESULT 4
Q9PVD2
ID Q9PVD2 PRELIMINARY; PRT; 542 AA.
AC Q9PVD2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE PARATHYROID HORMONE-RELATED PROTEIN RECEPTOR PTH3R.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99428481; PubMed=10497171;
RA Rubin D.A., Jueppner H.;
RT "Zebrafish Express the Common Parathyroid Hormone/Parathyroid Hormone-
RT related Peptide Receptor (PTH1R) and a Novel Receptor (PTH3R) That Is
RT Preferentially Activated by Mammalian and Fuguish Parathyroid
RT Hormone-related Peptide."
RL J. Biol. Chem. 274:28185-28190(1999).
DR EMBL; AF132085; AAF01266.2; -
DR InterPro; IPR000832; -
DR Pfam; PF00002; 7tm.2; 1.
DR PRINTS; PR00249; GPCRSECRETIN
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR SMART; SM00008; Hormr; 1.
KW Receptor.
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SQ SEQUENCE 542 AA; 61438 MW; 08688658E2727303 CRC64;
Query Match 45.0%; Score 1307.5; DB 13; Length 542;
Best Local Similarity 48.9%; Pred. No. 9.4e-101;
Matches 260; Conservative 84; Mismatches 123; Indels 65; Gaps 10;
QY 19 CUL--ARAQLSDSGYITIEQIVLVKAKVQCELMITAQLQ-EGEGNCFPEWDGLICWPR 75
Db 14 CVMGARALISDDVITRDEQIFLLIGARSCEIRAGSDVVRENCAPEWDGLICWPT 73
QY 76 GTVGKISAVPCPPYIYDFNHNKGVAFRHNCPNGTWFDMISLNTKNTWANSOCLRFLOPDISI 135
Db 74 GKPNOMVAVLCPYIYDFNHNKGVAFRHNCPNGTWFDMISLNTKNTWANSOCLRFLOPDISI 132
QY 136 KQOECERLYVMYTVGYSTISFGSLAVAILIIGYFRRLHCTRNVIHMLFVSPMLRATSF 195
Db 133 DOEVEFRRLYLMYITIGYSLAALLVAVSILCYFRRLHCTRNVIHMLFVSPMLRATSF 192
QY 196 VKDRVYVHAHIGVKELESLESLIMODDPONSIEATSVDKSQYIGCKIAYVMFYFLATNYWIL 255
Db 193 VKDAVLYAVTNDGELED-----GAVEQRPWVGCKAAVTLFLYLLATNHYWIL 239
QY 256 VEGLYLHNLIFVAFSFDTKYLMGFTLIGWGPFAAFVAAWAVARATLADARQWEISAGDIK 315
Db 240 VEGLYLHNLIFVAFSFDTKYLMGFTLIGWGPFAAFVAAWAVARATLADARQWEISAGDIK 299
QY 316 WYQAPILAAIAGLNFILNTVRVLATKIWETNAVGHDTKQYRKLAKSTLVLVLFVGVH 375
Db 300 WYQAPILAAIAGLNFILNTVRVLATKIWETNAVGHDTKQYRKLAKSTLVLVLFVGVH 359
QY 376 YIVFVCLPHS-FTGLGWEIRHCELFNSFGQFFVSIYCYCNGEVAQAEVKRMWSRWNL 434
Db 360 YMLFALPYDTVGLLQWQIOMHYEMLFNSQGFVAFIYCYCNGEVAQAEVKRMWSRWNL 419
QY 435 VDWKR-----TPPGSRRCGSVLTTHSTSSOSQVAAAHAWCLSLAKLPRSPADSUT 488
Db 420 LDLKQKARVSHSAGCGSGYGGMM--SHTTQ-----PGYAPQDTE 449
QY 489 TSLYLAGSVTQSRASHTLSTRNKEDSGRQDDILMEKPSRPMESNPDT 540
Db 450 -SVCLSVSGA---KGGHSLHTIGAGSHQSHGSL-----PGYAPQDTE 490

RESULT 5
Q9R1D4
ID Q9R1D4 PRELIMINARY; PRT; 169 AA.
AC Q9R1D4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE PARATHYROID HORMONE TYPE-2 RECEPTOR PRECURSOR (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99367425; PubMed=10438471;
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
RT "A G protein-coupled receptor from zebrafish is activated by human
RT parathyroid hormone and not by human or teleost parathyroid hormone-
RT related peptide. Implications for the evolutionary conservation of
RT calcium-regulating peptide hormones."
RL J. Biol. Chem. 274:23035-23042(1999).
DR EMBL; AF132083; AAD51909.1; -
DR InterPro; IPR000832; -
DR Pfam; PF00002; 7tm.2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
KW Receptor.
FT NON_TER 1 169
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SQ SEQUENCE 169 AA; 19674 MW; 748CC8231F1C69EA CRC64;

Query Match      29.5%; Score 858.5; DB 11; Length 169;
Best Local Similarity 92.9%; Pred. No. 6e-64;
Matches 158; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 250 NYWILVEGLYLNHLIFVAFSDTKYLMGFFPAFAVAAVARATLADARCWEL 309
D 1 NYWILVEGLYLNHLIFVAFSDTKYLMGFFPAFAVAAVARATLADARCWEL 60
QY 310 SAGDIKWIYQAPILAAIGLNFILNTVRLVATKIWETNAVGHDRKQYRKLA 369
D 61 SAGD-RWIIYQAPILAAIGLNFILNTVRLVATKIWETNAVGHDRKQYRKLA 119
QY 370 LVFGVHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGQFFVSIYCYCNGE 419
D 120 LVFGVHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGQFFVSIYCYCNGE 169

RESULT 6
QYVHC6 PRELIMINARY; PRT; 444 AA.
AC QYVHC6;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DE VASOACTIVE INTESTINAL PEPTIDE/PITUITARY ADENYLATE CYCLASE ACTIVATING
DE POLYPEPTIDE RECEPTOR.
OS Rana ridibunda (laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
ON NCBI_TaxID=8406;
RP SEQUENCE FROM N.A.
RC TISSUE=PITUITARY;
RA Alexandre D., Anouar Y.;
RT "A cloned frog VIP/PACAP receptor exhibits pharmacological and tissue
RT distribution characteristics of both VPAC1 and VPAC2 receptors in
RT mammals.";
RL Endocrinology 0:0-0(1999).
DR EMBL; AF100644; AAD03602.1; -.
DR InterPro; IPR000832; -.
DR Pfam; PF00002; 7tm2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G-PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G-PROTEIN_RECEP_F2_2; 1.
DR SMART; SM00008; Hornr; 1.
KW Receptor.
SQ SEQUENCE 444 AA; 50955 MW; 883B25B729314C4C CRC64;

Query Match      28.0%; Score 814; DB 13; Length 444;
Best Local Similarity 36.8%; Pred. No. 9.2e-60;
Matches 168; Conservative 73; Mismatches 133; Indels 82; Gaps 12;

QY 41 VLKAKVQCELNITAOLOEE-----GNCFFPEWDLGICWPRGTGKISAVPCPPY 89
D 17 ILCVPECSIMYQIELKHECEVNHEDYFNDTAVCKRTWDTNITCWFSASIGEYVVLQCPY 76
QY 90 IYDFNH---KGVAFRHCPNGTWDFMHSLNKTNWYNSDCLRFLOPDISIGKOE-FCERLY 145
D 77 FSNFTTGTGVNGVNSKNTSEG-WSEMYP-----ATYAAAGCFSTNDTPTPEQQTFFGAIK 130
QY 146 VMYTYGYSIFSGSLAVAILIIGYFRRLHCTRNYIHHLFLVSEMLRATSFIVKDRVV---- 201
D 131 TGTIGHISLUSLSLTAAMAILICFRKLHCTRNYIHHLFLVSEMLRAIAVFIKIDVIFESG 190
QY 202 ---HAHIGVKELESIMQDDPONSTEATSVDKSOYIGCKIAVVMFYFIATNYWILVEG 258
D 191 ESDHCHVG-----SVGCKAANVFQYCIANFFWLLVEG 224
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QY 259 LVHLNLIIVAFSDTKYLMGFFPAFAVAAVARATLADARCWELSGADIKWYI 318
D 225 LVHLNLIIVAFSDTKYLMGFFPAFAVAAVARATLADARCWELSGADIKWYI 284
QY 319 QAPILAAIGLNFILNTVRLVATKIWETNAVGHDRKQYRKLA 378
D 285 KTFPILVSLVNFILNTVRLVATKIWETNAVGHDRKQYRKLA 343
QY 379 FVCLPHSFTGLGWEIRHMCLEFNSFGQFFVSIYCYCNGEYQVAAEVKKWMSRWNL----S 434
D 344 FAFPPDNFK---VEVLVFEILGSGFQGVVAVLVCFLNGEYQVAAELKKRWNRNLERPMG 400
QY 435 VDWK-RTPPCGS-----RRCGS 450
D 401 KDMKYHHPHSLGSGNGTFTQISMLTKCSPKTRRCSS 436

RESULT 7
QYRLT8 PRELIMINARY; PRT; 459 AA.
AC QYRLT8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE VASOACTIVE INTESTINAL POLYPEPTIDE 1 (VPAC1) RECEPTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=129SVJ;
RA Hashimoto H., Nishino A., Shintani N., Hagihara N., Copeland N.G.,
RA Jenkins N.A., Yamamoto K., Matsuda T., Ishihara T., Nagata S.,
RA Baba A.;
RT "Genomic organization and chromosomal location of the mouse vasoactive
RT intestinal polypeptide 1 (VPAC1) receptor.";
RL Genomics 58:90-93(1999).
DR EMBL; AB022860; BAA81896.1; -.
DR EMBL; AB022848; BAA81896.1; JOINED.
DR EMBL; AB022849; BAA81896.1; JOINED.
DR EMBL; AB022850; BAA81896.1; JOINED.
DR EMBL; AB022851; BAA81896.1; JOINED.
DR EMBL; AB022852; BAA81896.1; JOINED.
DR EMBL; AB022853; BAA81896.1; JOINED.
DR EMBL; AB022854; BAA81896.1; JOINED.
DR EMBL; AB022855; BAA81896.1; JOINED.
DR EMBL; AB022856; BAA81896.1; JOINED.
DR EMBL; AB022857; BAA81896.1; JOINED.
DR EMBL; AB022858; BAA81896.1; JOINED.
DR EMBL; AB022859; BAA81896.1; JOINED.
DR InterPro; IPR000832; -.
DR InterPro; IPR001879; -.
DR Pfam; PF00002; 7tm2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G-PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G-PROTEIN_RECEP_F2_2; 1.
DR SMART; SM00008; Hornr; 1.
KW Receptor.
SQ SEQUENCE 459 AA; 52094 MW; C0C3A9AE1ADF611D CRC64;

Query Match      27.2%; Score 791.5; DB 11; Length 459;
Best Local Similarity 36.6%; Pred. No. 7.1e-58;
Matches 181; Conservative 81; Mismatches 145; Indels 87; Gaps 19;

QY 13 WLMGLSCULARA---QLSDSGTITIE-----EQIVLVKAKVQCELNITAOLOEEGNC 64
D 11 WL----CVLAGALACALGAPGSAASPHQCEYLMQIEKQROOCLEE--AQLENKTTGCS 64
QY 65 PWDGLICWPRGTGKISAVPCPPYIDFN--HKGVAFRHCNPNCTWDFMHSLNKTNWYI 122
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Db 65 KMDNLTCTWPTPWQVWVLDCLPLIFOLFSPHGYNISRNCTEEG-----WSQ- 112  
QY 123 SDCLRFLOP---DISG-----KQECERLYVMYTVGYSTISFGSLAVAILIG 167  
Db 113 -----LEPGYHIACGLNDRASMDDEQOQTEFYDAVKTGTIGYSLASLLVAMAILL 166  
QY 168 YFRLHCTRNYIHMHLFVSFMLRATSIYFKDRVVAHIGVKELESIMODDPQNSIEATS 227  
Db 167 LFRKLHCTRNYIHMHLFMSFILRATAVFIKDM-----ALFNGETDHCSEAS- 213  
QY 228 VDKSOYIGCKIAVWMFYIPLATNYWILVEGLYHLNLIYFAVFSDDTKYLGWFLILIGWGP 287  
Db 214 -----VSKAAVVFQYCYMANFFWLLVEGLYHLNLIYFAVFSDDTKYLGWFLILIGWGP 267  
QY 288 AAFVAAWAVARATLADARCE-LSAGDIKIYQAPILAAIGLNFILNTVVRVATKIWE 346  
Db 268 SVFIMTWIVRIHFEDFGCWDTIINSLSLWIKGPILISILVNFILFICIRILVOKLRP 327  
QY 347 TNAVGHDRKQYRKLAQSTLVLVFVGHYIVFVCLPHSFTGLGWEIRMHCELFNFSFOG 406  
Db 328 PD-IGKNDSSPYSLAKSTLLIPLFGVHVMPAFPPDNFKA---QVKMVFELVVGSGFOG 383  
QY 407 FVSIYCYNGEVOAEVKKMSRNLS--VDW--KRTPPCGSRR---CG---SVLTITVT 456  
Db 384 FVVAIYLCFLNGEVOAEELRRKRRWHLQGLVWGSKSQHPWGGSGNGYSCSTQVSMLTRVS 443  
QY 457 ----HSTSSOSOVA 466  
Db 444 PSARRSSFOAEVS 457

RESULT 8  
QYJ140  
ID Q9J140 PRELIMINARY; PRT: 459 AA.  
AC Q9J140;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE VASOACTIVE INTESTINAL PEPTIDE RECEPTOR TYPE 1.  
GN VIPRI.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N;  
RA Karacay B., O'Dorisio M.S., Kasow K., Krahe R.;  
RT "Cloning and Fine Mapping of the Vasoactive Intestinal Peptide  
Receptor 1 (VPAC1): A Comparative Analysis of Human, Rat and Murine  
genes";  
RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
RL EMBL: AF266282; AAF77053.1; -  
DR InterPro; IPR000832; -  
DR InterPro; IPR001879; -  
DR Pfam; PF00002; 7tm.2; 1.  
DR PRINTS; PR00249; GPCRSECRETIN.  
DR PROSITE; PS00649; G\_PROTEIN\_RECEPTOR\_F2\_1; 1.  
DR PROSITE; PS00650; G\_PROTEIN\_RECEPTOR\_F2\_2; 1.  
DR SMART; SM00008; Hormr; 1.  
KW Receptor.  
SQ SEQUENCE 459 AA; 52095 MW; 9D1ADF8567D4D7F CRC64;

Query Match 27.2%; Score 791.5; DB 11; Length 459;  
Best Local Similarity 36.6%; Pred. No. 7.le-58;  
Matches 181; Conservative 81; Mismatches 145; Indels 87; Gaps 19;  
QY 13 WMLGSCILARA---QLSDGTITIE---EQIVLVKAKVOCLELNTAQLOEGEGNCF 64  
Db 11 WL-----CVALACALGAPGASPHQECYLMIEKROOCLLEE---AQLENETTGS 64  
QY 65 PEWDGLICVPRGTGKISAVPCPPYIYDFN--HKGVAFRHCNPNGTWDFMHSINKTWANY 122

Db 65 KMDNLTCTWPTPWQVWVLDCLPLIFOLFSPHGYNISRNCTEEG-----WSQ- 112  
QY 123 SDCLRFLOP---DISG-----KQECERLYVMYTVGYSTISFGSLAVAILIG 167  
Db 113 -----LEPGYHIACGLNDRASMDDEQOQTEFYDAVKTGTIGYSLASLLVAMAILL 166  
QY 168 YFRLHCTRNYIHMHLFVSFMLRATSIYFKDRVVAHIGVKELESIMODDPQNSIEATS 227  
Db 167 LFRKLHCTRNYIHMHLFMSFILRATAVFIKDM-----ALFNGETDHCSEAS- 213  
QY 228 VDKSOYIGCKIAVWMFYIPLATNYWILVEGLYHLNLIYFAVFSDDTKYLGWFLILIGWGP 287  
Db 214 -----VSKAAVVFQYCYMANFFWLLVEGLYHLNLIYFAVFSDDTKYLGWFLILIGWGP 267  
QY 288 AAFVAAWAVARATLADARCE-LSAGDIKIYQAPILAAIGLNFILNTVVRVATKIWE 346  
Db 268 SVFIMTWIVRIHFEDFGCWDTIINSLSLWIKGPILISILVNFILFICIRILVOKLRP 327  
QY 347 TNAVGHDRKQYRKLAQSTLVLVFVGHYIVFVCLPHSFTGLGWEIRMHCELFNFSFOG 406  
Db 328 PD-IGKNDSSPYSLAKSTLLIPLFGVHVMPAFPPDNFKA---QVKMVFELVVGSGFOG 383  
QY 407 FVSIYCYNGEVOAEVKKMSRNLS--VDW--KRTPPCGSRR---CG---SVLTITVT 456  
Db 384 FVVAIYLCFLNGEVOAEELRRKRRWHLQGLVWGSKSQHPWGGSGNGYSCSTQVSMLTRVS 443  
QY 457 ----HSTSSOSOVA 466  
Db 444 PSARRSSFOAEVS 457

RESULT 9  
QYJBG2  
ID Q9JBG2 PRELIMINARY; PRT: 418 AA.  
AC Q9JBG2;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE VASOACTIVE INTESTINAL PEPTIDE RECEPTOR (FRAGMENT).  
GN CVIPR.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kansaku N., Shimada K., Saito N., Arakawa K., Suzuki T., Matsuda Y.,  
Zadworny D.;  
RT "Molecular cloning of chicken VIP receptor cDNA, tissue distribution  
and chromosomal localization";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB029895; BAA95164.1; -  
DR InterPro; IPR000832; -  
DR InterPro; IPR001879; -  
DR Pfam; PF00002; 7tm.2; 1.  
DR PRINTS; PR00249; GPCRSECRETIN.  
DR PROSITE; PS00649; G\_PROTEIN\_RECEPTOR\_F2\_1; 1.  
DR PROSITE; PS00650; G\_PROTEIN\_RECEPTOR\_F2\_2; 1.  
DR SMART; SM00008; Hormr; 1.  
KW Receptor.  
FT NON\_TER  
SQ SEQUENCE 418 AA; 48191 MW; 7AE4796ADCB08FF3 CRC64;

Query Match 26.8%; Score 780.5; DB 13; Length 418;  
Best Local Similarity 37.1%; Pred. No. 5.3e-57;  
Matches 166; Conservative 76; Mismatches 138; Indels 67; Gaps 14.  
QY 32 ITTEEQLVLVKKAKVOCLELNTAQLOEGEGNCFEWDGLICVPRGTGKISAVPCPPYI- 90  
Db 3 LEIEEE-----RSQCLAEITEDNQ--TSGCRROWDNITCWAQVGVVVKPCPKYFR 53

us-09-236-468a-2.rspt

Mon Sep 24 09:54:53 2001

```

171 KHLCTRNFIHMLNFVSMFLRAISVFIKDGVLXA-----EDSDHCFVHT--- 215
230 KSOYIGKIAVVMFYELATNYWILVEGLYHNLIFVAFSTDYKYLNGFILIGWGPAA 289
216 ---VGCKRAVWVFHYCVMSNYFWLFIIEGLYLTLLVETFFPFRYFYWTIIGWGTPTI 271
290 FVAANAVARATLADARCWELSAGD-TKWIYQAPILAAIGLNFILNTVVRVATKWIETN 348
272 CVTIWAVLRUHFDDSGCWMNDNTALWVVKGPVASIMINFLVFIIGIILVQKL-QSP 330
349 AVGHDTRKQYKRLAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRHMCLEFFNSQGF 408
331 DIGNESSIYLRARSTLILPLFGIHVTFVAFSPEDSK---RRLVFEGLGSGFQFV 387
409 VSIICYCNGEQAQVKKMWSRWNL---SVDWK--RTPPCGSRRC-GSVLTVTHSTSS 461
388 VAVLCFLNGEQSEIKRKRWSWTNRYFAVDLKOQRHPSLASSGVNGGTQLSILSKSS 447
462 QSOVAAAHAWCLSLAKLP 479
448 QIRMSSPLAETVNL-NLP 464

RESULT 11 PRELIMINARY: PRT: 438 AA.
ID 073768
AC 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 16, Last annotation update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GROWTH-HORMONE RELEASING HORMONE-LIKE PEPTIDE RECEPTOR.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariorhynchi;
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
OC NCBI_TaxID=7957;
OX [1]
RP SEQUENCE FROM N.A.
RA Chan K.W., Yu K.L., Rivier J., Chow B.K.C.;
RL Neuroendocrinology 0:0-0(1998).
RL EMBL: AF048819; AAC15698.1; -
DR InterPro: IPR000832; -
DR InterPro: IPR001879; -
DR Pfam: PF00002; 7tm.2; 1.
DR PRINTS: PR00249; GPCRSECRETIN.
DR PROSITE: PS00650; G_PROTEIN_RECEP_F2.2; UNKNOWN_1.
DR SMART: SM00008; Hormr. 1.
DR SEQUENCE 438 AA: 50305 MW: C3516A52D692C339 CRC64;
SQ
Query Match 24.2%; Score 702.5; DB 13; Length 438;
Best Local Similarity 35.5%; Pred. No. 1.7e-50;
Matches 148; Conservative
57 QEGEGNCFPEWMDGLICWPRGTGKISAVPCPP-YIYDFNHKGVAFHCHNPNGTWDFMHL 115
55 QSQOQCTWTDWGIKRCWQAKTAKTQGLINVCSDVDFQHSNTQGFYRNCSSNG-W----- 107
116 NKTWANYSDCLRFQPDISIGKQFCERLYRVMYTVGYSISFGSLAVAILIIGYFRRLLHCT 175
116 NKTWANYSDCLRFQPDISIGKQFCERLYRVMYTVGYSISFGSLAVAILIIGYFRRLLHCT 167
108 SDPYSEAEACTFDDSESGTSTVSTLTSLKQLYTAGYATSLISLITAVIIFTCRKHCT 235
176 RNYIHMHLFVSGFMRATRSIFVKDRVVAHIGVKELESIMODDPQNSIATSVDRKSOYIG 208
168 RNYIHINLVFVSEILRATAVFIKDAY-----LFSDETQNHCLMSIV-----A 208
236 KQIAVVMFYELATNYWILVEGLYHNLIFVAFSTDYKYLNGFILIGWGPAAVANA 295
209 CKTAVTFQFCILNTNYFWLLVEGLYLTLLVETFFPFRYFYWTIIGWGTPTI 268
296 VARATLADARCWELSAG-DIKWIYQAPILAAIGLNFILNTVVRVATKWIETN 354
269 LTRQFYDNRGCGDDTDNNNIWILKGPITVSLIANIILFNLIRILVOKLSPGVGGNDT 328

Query Match 24.5%; Score 713; DB 13; Length 465;
Best Local Similarity 35.6%; Pred. No. 2.5e-51;
Matches 156; Conservative
58 EGEENCFPEWMDGLICWPRGTGKISAVPCPPYIYDF-----NHKGVAFHCHNPNGTWDFM 113
65 DGFKEPCPEWMDGLICWPRGTGKISAVPCPPYIYDF-----LFDMSPEEGPKIRNCTFFG-W---- 118
114 SLNKTWANYSD-CL---RELQPDISIGKQFCERLYRVMYTVGYSISFGSLAVAILIIGYF 169
119 --SESPHYVDACMIGENTKPKDM-----YYASVKAIVTVGYSISLVSUTTAMVILCRF 170
170 RRLHCTRNFIHMLNFVSMFLRAISVFIKDGVLXA-----EDSDHCFVHT--- 215
171 KHLCTRNFIHMLNFVSMFLRAISVFIKDGVLXA-----EDSDHCFVHT--- 215

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Query Match	23.6%	Score	685.5;	DB	13;	Length	465;
Best Local Similarity	32.1%	Pred.	No. 4.9e-49;				
Matches	157;	Conservative	97;	Mismatches	168;	Indels	67;
Gaps	14;						
Qy	13	WLMGSLCLARAQLDSDGTTITIEQIVLVKAKVQ-CELNITAOLOEGEGNCFFPEWDGLI	71				
Db	8	FLLLGFWASQVASHPHYCIIKKEEACL--EKIQRYEIEMNWDTQSQ--CPGMDWNI	61				
Qy	72	CWPRGTGKISAVPCPPY-----IYDFNHKGVAFRHCNPNGT	108				
Db	62	CWMPAEVGVKVSVRCPALFSMIGSEDEMDFVDRSLGWSPENIEEQSQSGTIKRNCTENG-	120				
Qy	109	WDFMHSLNKWTANYSDCLURFLQDLSIGKQBFERLYVWTVGVYSISFGSLAVAILI	168				
Db	121	W-----SEPPHYSEACDFDINETGPDQDQYYISVKALYTVGVYSTVALVTTAMVILCR	174				
Qy	169	FRRLCHCTRNYTHMHLFVSFMLRATSFYVKVRVVAHIGVKELESIMODDPQNSTEATSV	228				
Db	175	FRKLCHCTRNFTHMNLFVSFILRAISVFTKDEVLAE-----QDN--NHCHLSTV	221				
Qy	229	DKSQYIGCKIAVWAFIYELATNYIWLVEGLYIHLNLIFFAVAFSDTKYLWGFILIGWGPPA	288				
Db	222	E-----CKVMVFFHYCVMSNYFWLFTIEGLYFTLLVETPEPERRYFWYTIIGMGTP	275				
Qy	289	AFVAAVAVARATLADARCWELISAG-DIKWTVQAPILAAIGLNFILFLNTVRVLATKI	347				
Db	276	ICVTIVAVLRHLFONLGCWDDNNNTGLMWWYIKGPGYIGSIMINFLVFGIILIVLQKL-QS	334				

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Query Match      21.9%; Score 636; DB 6; Length 423;
Best Local Similarity 30.9%; Pred. No. 5.8e-45;
Matches 149; Conservative 88; Mismatches 163; Indels 82; Gaps 15.;

Qy    10 VVGWMLMGSCLLARAQLSDGTTIEBQIVLVILKAKVQCCELNITAOLOEGNCFFPE-- 66
Db    5 VWGACVL--CLL-----GPLP-----VLGHVHPEDCVITQRDEQAQLAAEG 47

Qy    67 -----WDGLICMPRGTVGKI SAVPCPPYIYDFNHK -GVAFRHCNPNGTWFDMHS 114
Db    48 MPNSTLGCPRIWDGLLCWPATSGEWSLPCPAFFSHFSSEP GAVKRDCITIAG-W----- 101

Qy    115 LNKWTANYSDCLRFLQDPDISIGKEFCERLYVMYVTGYSISFGSLAVAIIIGYFRRLHC 174
Db    102 -SEFPYPYPEACP-VPLELTTEEEKSYSAVR IITVGMHVSAAALLVAIIILVALRLHC 159

Qy    175 TRNTIWHHLFVSFMLRATSIFVKDRVVHAHIGVKELESIMQDDPONSIEATSVDKSQYI 234
Db    160 PRNIHTQLFITFILKAANVPLKD-----ATLFHQENTDHCSEST-----V 200

Qy    235 GCKIAVVMFYIFLATNYWYLVEGLYLHNLI FVAFFSDTKYLMGFILLIGNFFPAFVAAM 294
Db    201 LCKYSVATSFHEATWNFTNSWLLAEAVILTCLLVSTPRRRVFWMLVLAANGLP LLTGTMM 260

Qy    295 AVARATLADARCWEL-SAGDIKWIKYQAPILA AIGNLFIPLNTVRVLATKIWETNAVGDH 353
Db    261 VGCKLAFEDVACWLDGDSPPYWMIIKGPI VLUSGVGNFGLEFINIRILLRKLEPTQGS LH- 319

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Db 320 TQOYWRLSKSTLLIPLFGIHYVIFNLPDS---AGLDIRLPLELGLGSFQGFIVAILY 376  
Qy 414 CYCNGEVOAEV 424  
|: | | | |  
Db 377 CFLNQEVTPV 387

Search completed: September 21, 2001, 17:09:25  
Job time: 198 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 21, 2001, 16:52:17 ; Search time 14.43 Seconds  
(without alignments)  
771.960 Million cell updates/sec

Title: US-09-236-468A-2  
Perfect score: 2907  
Sequence: 1 MAWLGLSLHVMGWLMLGSL.....DDILMEKPSRPMESNPDTG 541

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2907	100.0	541	3	US-08-468-011A-2
2	2907	100.0	541	5	PCT-US95-07085-2
3	1397	48.1	585	1	US-08-142-439A-6
4	1397	48.1	585	2	US-08-869-477-6
5	1392	47.9	585	2	US-08-142-551B-125
6	1392	47.9	585	2	US-08-468-249A-19
7	1388	47.7	515	2	US-08-468-249A-18
8	1331.5	45.8	591	2	US-08-468-249A-20
9	1331.5	45.8	593	2	US-08-468-249A-21
10	801	27.6	449	1	US-08-142-439A-5
11	801	27.6	449	2	US-08-869-477-5
12	785	27.0	458	1	US-08-112-817C-2
13	773	26.6	1324	2	US-08-811-897A-56
14	713.5	24.5	437	2	US-08-538-816A-2
15	713.5	24.5	437	2	US-09-076-651-2
16	704	24.2	431	2	US-08-538-816A-9
17	704	24.2	431	2	US-09-076-651-9
18	702.5	24.2	438	2	US-08-538-816A-1
19	702.5	24.2	438	2	US-09-076-651-1
20	696.5	24.0	448	2	US-08-811-897A-18
21	696.5	24.0	448	2	US-08-855-213-18
22	696.5	24.0	467	2	US-08-811-897A-19
23	696.5	24.0	467	2	US-08-855-213-19
24	689.5	23.7	525	2	US-08-811-897A-23
25	689.5	23.7	525	2	US-08-855-213-23
26	688.5	23.7	448	2	US-08-811-897A-16
27	688.5	23.7	448	2	US-08-855-213-16

28	688.5	23.7	485	2	US-08-811-897A-17	Sequence 17, Appl
29	688.5	23.7	485	2	US-08-855-213-17	Sequence 17, Appl
30	684.5	23.5	448	2	US-08-811-897A-22	Sequence 22, Appl
31	684.5	23.5	448	2	US-08-855-213-22	Sequence 22, Appl
32	681.5	23.4	476	2	US-08-811-897A-20	Sequence 20, Appl
33	681.5	23.4	476	2	US-08-855-213-20	Sequence 20, Appl
34	681.5	23.4	495	2	US-08-811-897A-21	Sequence 21, Appl
35	681.5	23.4	495	2	US-08-855-213-21	Sequence 21, Appl
36	675	23.2	552	2	US-08-811-897A-27	Sequence 27, Appl
37	675	23.2	552	2	US-08-855-213-27	Sequence 27, Appl
38	674.5	23.2	553	2	US-08-811-897A-25	Sequence 25, Appl
39	674.5	23.2	553	2	US-08-855-213-25	Sequence 25, Appl
40	673.5	23.2	476	2	US-08-811-897A-14	Sequence 14, Appl
41	673.5	23.2	476	2	US-08-855-213-14	Sequence 14, Appl
42	673.5	23.2	513	2	US-08-811-897A-15	Sequence 15, Appl
43	673.5	23.2	513	2	US-08-855-213-15	Sequence 15, Appl
44	672.5	23.1	553	2	US-08-811-897A-29	Sequence 29, Appl
45	672.5	23.1	553	2	US-08-855-213-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1  
US-08-468-011A-2  
; Sequence 2, Application US/08468011A  
; Patent No. 6030804  
; GENERAL INFORMATION:  
; APPLICANT: Soppet, Daniel R  
; APPLICANT: Yi, Li  
; APPLICANT: Rosen, Craig A  
; APPLICANT: Ruben, Steven  
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor  
; TITLE OF INVENTION: HLTG974  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,  
; ADDRESSEE: Stewart & Olstein  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07068-1739  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,011A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 541 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-468-011A-2

Query Match 100.0% Score 2907; DB 3; Length 541;  
Best Local Similarity 100.0%; Pred. No. 2.5e-294;  
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAWLGLSLHVMGWLMLGSLARQLDSGTITIEQIVLVKAKVQCELNITAIQLQCE 60

Db 1 MAWLASLHVWGLMGLSCLLARAQSDSGTITIEEQIVLVKAKVQCELNITAQLEGE 60  
QY 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIYDFNHHKGVAFRHCNPNGTWDFMHSLNKTTWA 120  
Db 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIYDFNHHKGVAFRHCNPNGTWDFMHSLNKTTWA 120  
QY 121 NYSDCRLRFQPDISIGKQECERLYVMYTVGYISFGSLAVAILIIGYFRRHLCHTRNYIH 180  
Db 121 NYSDCRLRFQPDISIGKQECERLYVMYTVGYISFGSLAVAILIIGYFRRHLCHTRNYIH 180  
QY 181 MHLFVSFMLRATSIYKDRVVAHIGVKELESIMODDPONSTEATSVDKSQYIGCKIAV 240  
Db 181 MHLFVSFMLRATSIYKDRVVAHIGVKELESIMODDPONSTEATSVDKSQYIGCKIAV 240  
QY 241 VMEIYFATNYWILVEGLYLNHLIEVAFSDTKYLGWFGFLLIGWGPAAFAVAWAVARAT 300  
Db 241 VMEIYFATNYWILVEGLYLNHLIEVAFSDTKYLGWFGFLLIGWGPAAFAVAWAVARAT 300  
QY 301 LADARCWELSGADIKWIYQAPILAAIAGLNFILPLNTVRVLATKIWETNAVGHDTKQYRK 360  
Db 301 LADARCWELSGADIKWIYQAPILAAIAGLNFILPLNTVRVLATKIWETNAVGHDTKQYRK 360  
QY 361 LAKSTLVVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFNSFGQFFVSIYCYCNGEV 420  
Db 361 LAKSTLVVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFNSFGQFFVSIYCYCNGEV 420  
QY 421 QAEVKKMSRWNLSDWKRTPPCGSRRCGSLVLTVTHTSSQSQVAAAHAHAWCLSLAKLPR 480  
Db 421 QAEVKKMSRWNLSDWKRTPPCGSRRCGSLVLTVTHTSSQSQVAAAHAHAWCLSLAKLPR 480  
QY 481 SPADSLTATSLYLAMSGVTSQRTASHTLSTRSNKEDSGRQDDILMEKPSRPMESNPDT 540  
Db 481 SPADSLTATSLYLAMSGVTSQRTASHTLSTRSNKEDSGRQDDILMEKPSRPMESNPDT 540

RESULT 2

PCT-US95-07085-2  
; Application 2, Application PC/TUS9507085  
; GENERAL INFORMATION:  
; APPLICANT: Soppet, Daniel R  
; APPLICANT: Yi, Li  
; APPLICANT: Rosen, Craig A  
; APPLICANT: Ruben, Steven  
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor  
; TITLE OF INVENTION: HLTG74  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07068-1739  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/07085  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-393  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 541 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-07085-2  
  
Query Match . 100.0%; Score 2907; DB 5; Length 541;  
Best Local Similarity 100.0%; Pred. No. 2.5e-294;  
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MAWLASLHVWGLMGLSCLLARAQSDSGTITIEEQIVLVKAKVQCELNITAQLEGE 60  
Db 1 MAWLASLHVWGLMGLSCLLARAQSDSGTITIEEQIVLVKAKVQCELNITAQLEGE 60  
QY 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIYDFNHHKGVAFRHCNPNGTWDFMHSLNKTTWA 120  
Db 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIYDFNHHKGVAFRHCNPNGTWDFMHSLNKTTWA 120  
QY 121 NYSDCRLRFQPDISIGKQECERLYVMYTVGYISFGSLAVAILIIGYFRRHLCHTRNYIH 180  
Db 121 NYSDCRLRFQPDISIGKQECERLYVMYTVGYISFGSLAVAILIIGYFRRHLCHTRNYIH 180  
QY 181 MHLFVSFMLRATSIYKDRVVAHIGVKELESIMODDPONSTEATSVDKSQYIGCKIAV 240  
Db 181 MHLFVSFMLRATSIYKDRVVAHIGVKELESIMODDPONSTEATSVDKSQYIGCKIAV 240  
QY 241 VMEIYFATNYWILVEGLYLNHLIEVAFSDTKYLGWFGFLLIGWGPAAFAVAWAVARAT 300  
Db 241 VMEIYFATNYWILVEGLYLNHLIEVAFSDTKYLGWFGFLLIGWGPAAFAVAWAVARAT 300  
QY 301 LADARCWELSGADIKWIYQAPILAAIAGLNFILPLNTVRVLATKIWETNAVGHDTKQYRK 360  
Db 301 LADARCWELSGADIKWIYQAPILAAIAGLNFILPLNTVRVLATKIWETNAVGHDTKQYRK 360  
QY 361 LAKSTLVVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFNSFGQFFVSIYCYCNGEV 420  
Db 361 LAKSTLVVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFNSFGQFFVSIYCYCNGEV 420  
QY 421 QAEVKKMSRWNLSDWKRTPPCGSRRCGSLVLTVTHTSSQSQVAAAHAHAWCLSLAKLPR 480  
Db 421 QAEVKKMSRWNLSDWKRTPPCGSRRCGSLVLTVTHTSSQSQVAAAHAHAWCLSLAKLPR 480  
QY 481 SPADSLTATSLYLAMSGVTSQRTASHTLSTRSNKEDSGRQDDILMEKPSRPMESNPDT 540  
Db 481 SPADSLTATSLYLAMSGVTSQRTASHTLSTRSNKEDSGRQDDILMEKPSRPMESNPDT 540  
QY 541 G 541  
Db 541 G 541  
  
RESULT 3  
US-08-142-439A-6  
; Sequence 6, Application US/08142439A  
; Patent No. 5670360  
; GENERAL INFORMATION:  
; APPLICANT: Thorens, Bernard  
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1  
; TITLE OF INVENTION: (GLP-1)  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5670360o No. 5670360th America, Inc.  
; STREET: 405 Lexington Avenue, Suite 6400  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10174-6201  
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142.439A
; FILING DATE: 24-NOV-93
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; FILING DATE: 25-MAR-92
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Didelphis virginiana
; US-08-142-439A-6

Query Match 48.1%; Score 1397; DB 1; Length 585;
Best Local Similarity 48.0%; Pred. No. 6.4e-137;
Matches 275; Conservative 94; Mismatches 134; Indels 70; Gaps 10;

Qy 24 AQLSDGTTITTEEQIVLVKAKVOCENLIT----- 53
| : : | | | | | : : | | :
Db 24 ALVDADDVITTEEQIILLRNAQACEQRLKEVLRVPELAESAADMWRSASAKTKKEKPAEK 83
| : : | | | | | : : | | :

Qy 54 --AQLQEG-----EGNCFPEWDGLICWPRTGVGKISAVPCPPYIYDFNHHKGVAFR 101
| : : | | | | | : : | | :
Db 84 LYSQAEESREVSRSRLQDGFCLPEWDNIVCWPAGVPCVKVAVPCPDYIYDFNHHKGRAVR 143
| : : | | | | | : : | | :

Qy 102 HCNPNGTWDFMHSLNKWTANYSDCLRFLOPDISIGKQCEFCERLYVYTVGYISIFGSLAV 161
| : : | | | | | : : | | :
Db 144 RCDNSGMSWELVPGNNRTWANYSECYKFTNETR--EREVDFRLGMIYTVGYISISLGLTV 201
| : : | | | | | : : | | :

Qy 162 AILIGYERFLHCTNYTHMLFVSEMLRSTISIFVKDRVVAHIGVKELESIMODDPQN 221
| : : | | | | | : : | | :
Db 202 AVLLIGYERFLHCTNYTHMLFVSEMLRSTISIFVKDRVVAHIGVKELESIMODDPQN 260
| : : | | | | | : : | | :

Qy 222 SIEATSDVKSOYIGCKIAVVMFYIATNYWILVEGLHNLIFVAFSOTKYLWGFIL 281
| : : | | | | | : : | | :
Db 261 FTEPPADKAGVGRVAVTVFLVLTNTYVWILVEGLHNLIFVAFSOTKYLWGFIL 320
| : : | | | | | : : | | :

Qy 282 IGWGFPAFVAWAARATLADARCWELSGADIKWIYQAPILAAIGLNFILNTVRVLA 341
| : : | | | | | : : | | :
Db 321 FGWGLPAFVAWAARATLADARCWELSGADIKWIYQAPILAAIGLNFILNTVRVLA 380
| : : | | | | | : : | | :

Qy 342 TKIWTNAVGHDTKQYRKALKSTLVLVFVGVHVIYVPCVLPSS--FTGLGWEIRMHCELF 400
| : : | | | | | : : | | :
Db 381 TKLRETNAGRCDDTQYRKALKSTLVLVFVGVHVIYVPCVLPSS--FTGLGWEIRMHCELF 440
| : : | | | | | : : | | :

Qy 401 FNSQGFVSVIYCYNGEVOAEVKKMSRWNLSDWKRTPPCGSRRCGSLVTTVTH--- 457
| : : | | | | | : : | | :
Db 441 FNSQGFVSVIYCYNGEVOAEVKKMSRWNLSDWKRTPPCGSRRCGSLVTTVTH--- 493
| : : | | | | | : : | | :

Qy 458 -STQSQOVAHAHAWCLSLAKLPSPADSLTATSLYLAWSGTQSRATSHLTSTRNKED 516
| : : | | | | | : : | | :
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Qy	102	HCNPNGTWFHSLNKTWANY	SCLRFLPADDISIGKQFCERLYMYVTGY	SISFGSLAV	161
Db	144	RCDNSGWEIPLVPGNNRTWANY	SECVFLNETR--BREVDFRLGMYTGY	SISGLSTGY	201
Qy	162	AAILIGYFRRLHCTRNY	IHMHLFVSEFMRATSI	FFVDRVYVHAHIGVKEESLIMODDPON	221
Db	202	AVLILGYFRRLHCTRNY	IHMHLFVSEFMRARVSI	FIKDAVLYSOVSTDEIER--ITGEELRA	260
Qy	222	SIEATSDYCKQYIGCKTAVVMY	FIYFATNYWYLVEGLYLHNL	FIYAFSDFTQYKWLGFLL	281
Db	261	FTEPPPADKAGFVGRVAV	VFYFLYFTTNYWYLVEGLYLHSL	FIYAFSEKKYKWLGFLL	320
Qy	282	IGNGFPAAFVAANAVALATLADAR	CHWELSGADIKWYIQAPILAA	ATCLNFIELFNVRVLA	341
Db	321	FGMLPFAVFVAWVYVRATLANT	TECDLSGNKKWIIQIIVPILAA	VIVNFILINTIRVLA	380
Qy	342	TKIWTETNAUGHDRTKOYRK	LAKSTLVLVVFVGHYIVFVCLPHS	-FTGLGWIRMHCELF	400
Db	381	TKLRETNAGRCDTRQQYRK	LKLLKSTLVLPLFGVHYIVFNATPY	TEVSGILWQVQMYEML	440
Qy	401	FNSFQGFVFSIIYCYCNGE	VOAEVKKWRSRWNL	SVDWKFTPCGSRRCOSVLTVTYTH---	457
Db	441	FNSFQGFVAIIYCFNGE	VOAEIKKWSRWTLALDF	KRKARSGS-----STYSGYPM	493
Qy	458	-STSSQSOVAAAAHWCLSLAK	LPRSPADSLTATSLYLAMSGVYT	QTSRASHLTSTRSNKD	516
Db	494	VSHTSVTNVGPRGLAISLS--	PRLAPGACASANGHHQLPGVY	KHGSISEN-SLPSSGPE	550
Qy	517	SGRQRDDILM-----	EXKSPRPMESNPDT	539	
Db	551	PGYKDDCYLNGSLGYP	PMVWGQPPPLLEERET	583	

## RESULT

```

US-08-142-551B-125
; Sequence 125, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..585
; OTHER INFORMATION: /note= "PTH receptor"
US-08-142-551B-125

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Query Match	47.9%;	Score 1392;	DB 2;	Length 585;
Best Local Similarity	47.8%;	Pred. No. 2.1e-136;		
Matches 274;	Conservative 92;	Mismatches 137;	Indels 70;	Gaps
Qy	24	AOLDSDGTTITEQIVLVAKVQCELNITAOIQEGE-----	60	
Db	24	ALVDADDVITKEQIILIRNAQAQCRUKVEVURVPELAESA	83	
Qy	61	-----GNCPEWDGLICWPRGTGVKISAVCPYPPIYDF	101	
Db	84	LYPQAESEVSDRSRLQDGFCLPEWDNIVCPAGVPGKVVAV	143	
Qy	102	HCNPNGTWDPMHSLNKTWANYSOCLRFQLPDISIGKQFCER	161	
Db	144	RCDNSGWEIIVPGNNRTWANYSECVKFLNETR--BREVFDRL	201	
Qy	162	AILLIGVFRLLHCTRNIHMHLFVSMPLRATSFVKDRVVAHIG	221	
Db	202	AVLLIGVFRLLHCTRNIHMHLFVSMPLRAVSIFIKADVLSGV	260	
Qy	222	SIEATSVDKSQYIGCKTAVVMFYFATNYYTWLVLEGLYHNL	281	
Db	261	FTEPPADKAGFGCRVAVTVFLYFTNTYTWLVLEGLYHLSL	320	
Qy	282	IGWGFPAFVAANAVARATLADARCHELSAGDIKWIYQAPILA	341	
Db	321	FGWGLPAFVAVVMVTVRANTTECDLDSGNKKWIIQIIVPILA	380	
Qy	342	TKIWEITNAUGHDRKQYRKLAESTLVLVFGVHYIVFVCLPHS	400	
Db	381	TKLRETNAGRCDTRQYRKLLKSTLVLMPLFGVHYIVEMATPY	440	
Qy	401	FNSFGQFVSIYYCYNGEVOAEVKMMWSRNLSVDWKRTPPCG	457	
Db	441	FNSFGQFVAIYYFCNGEVOAEIKKWSRWTLALDFKRAKSGS	493	
Qy	458	-STSSQSOVAAAAHWCLSLAKLPRSPADSLTATSLYLA	516	
Db	494	VSHTSVTNVGRGLALSLS--PRLAPGACASANGHQHLP	550	
Qy	517	SGRQRDILM-----EKSPRPMESNPDT	539	
Db	551	PGTKDDCYLNGSLGYEPMWGEOPPPLEBERET	583	

## RESULT 6

US-08-468-249A-19  
; Sequence 19, Application US/08468249A  
; Patent No. 5886148  
; GENERAL INFORMATION:  
; APPLICANT: Segre et al., Gino V.  
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA  
; NUMBER OF SEQUENCES: 21  
; TITLE OF INVENTION: ENCODING SAME  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston







TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 593 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-468-249A-21

Query Match 45.8%; Score 1331.5; DB 2; Length 593;  
Best Local Similarity 47.4%; Pred. No. 4.3e-130;  
Matches 276; Conservative 80; Mismatches 135; Indels 91; Gaps 11;  
22 ARAQLSDGTTIEQIVLVKAKVQCELNITAQLQ----- 57  
Db 22 AYALVDADDVMTKEQIFLLHRAQCEKRLAEVLQRPASIMESDKGWTSASTGSKPRKD 81  
QY 58 -----EGEGN-----CPPEWDGLICWPRGTGKISAVPCPPYIYDFNHK 96  
Db 82 KASGKLYPESEEDKEAPTGSRYGRPCLPEDWDHILCPLGAPGEVAVPCPDYIYDFNHK 141  
QY 97 GVAFRHCNPGTWDFMHSLSLNTWYNSDCLRFQLQDISIGKQEFCEFLYVMTYVGSISF 156  
Db 142 GHAYRCDRNGSWELVPGHNRTWANYSECVKELTNETR--EREVDRLGMIYTVGSVSL 199  
QY 157 GSLAVAILIIGFRLHCTRTNIHMLFVSEMLRATSFVKDRVVAHIGVKLESL--- 213  
Db 200 ASLTAVAVLFLAYFRLHCTRTNIHMLFSLFMLRAVSIFVKDAVLYSGATLDEAERLTEE 259  
QY 214 ----TWQDDPQNSIEATSDVKSOYTGCKIATVVMFYFIATNYIWLVEGLYHNLIFVAF 269  
Db 260 ELRAITAQAPPPATAAG-----YAGCRVAVTFYFLYATNYIWLVEGLYHLSLIFNAF 314  
QY 270 FSDTYLNGFLIGGFPAFVAANAVARATLADARCWELSGDIKTIYQAPILAAIGLN 329  
Db 315 FSEKYLWGFVFGGLFAVFVAWVSVRATLANTGCDLSSGNKKKIYQVILASIVLN 374  
QY 330 FILFNTVRLATKIWEYNAVGHDRKQYKRLAKSTLVLVLFVGVHYIVFVCLPHS-FTG 388  
Db 375 FILFINVRLATKQRETNAGRCDFRQYKRLKSTLVLMPLFVGVHYIVFMATPYTEVSG 434  
QY 389 LGWETRMHCELFNFSGQFFVSIYCYNGEVOAEVKKMWSRWNLSDVMKRTPPGCSRR 448  
Db 435 TLWQVMHVEMLFNSFGQFFVSIYCYNGEVOAEVKKMWSRWNLSDVMKRTPPGCSRR 494  
QY 449 G-SVLTTHSTSSQSOVAHAHCLSLAKLPRSPADSLTATSL-YLAMSGVTQSRT-AS 505  
Db 495 SYGPMVSHTSVTVNGPRVGLG-----LPLSPRLPTATTNGHPQLPGHAKPGTAL 545  
QY 506 HTLSTRS-----NKEDSGRDRDDILMEK 528  
Db 546 ELETTPPAMAAPKDDGFLNGSCSLDEASGPERPPALLQE 587

RESULT 10  
US-08-142-439A-5  
Sequence 5, Application US/08142439A  
Patent No. 5670360  
GENERAL INFORMATION:  
APPLICANT: Thorens, Bernard  
TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1  
TITLE OF INVENTION: (GLP-1)  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESS: No. 5670360o No. 5670360disk of No. 5670360th America, Inc.  
STREET: 405 Lexington Avenue, Suite 6400  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10174-6201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/142.439A  
FILING DATE: 24-NOV-93  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 398/92  
FILING DATE: 25-MAR-92  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/00697  
FILING DATE: 23-MAR-93  
ATTORNEY/AGENT INFORMATION:  
NAME: Harrington, James J.  
REGISTRATION NUMBER: 38,711  
REFERENCE/DOCKET NUMBER: 3756.204-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 867 0123  
TELEFAX: 212 867 0298  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 449 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Rattus norvegicus  
STRAIN: Sprague-Dawley  
US-08-142-439A-5

Query Match 27.6%; Score 801; DB 1; Length 449;  
Best Local Similarity 37.3%; Pred. No. 5.4e-75;  
Matches 176; Conservative 81; Mismatches 149; Indels 66; Gaps 15;  
QY 14 LMLGSCLLARQALSDGTTIEQIVLVKAKVQCELNITAQL-OBEGNCFPE----- 66  
Db 12 LLLRLLLLTKAA-----HTVGVPRLCDVRRVLLLEHRAHCLQQLSKKKGALGPETASGE 67  
QY 67 --WDGLICWPRGTGKISAVPCPPYIYDFNHK-GVAFRHCNPGTWDFMHSLSLNTWYNS 123  
Db 68 GLWDMNSCWPSAPARTVEVQCPKFLMLSNKNGSLFRNCTQDG-----WSE--- 114  
QY 124 DCLRFQLQDISIG---KQEFCE-----LYVMYTVGYSISFGSLAVAILIIGYFRLH 173  
Db 115 ---TEPRDLAGVNNINNSFNERRHAYLLKLVMTYVGYSSSLAMLLVALSILCSFRLH 171  
QY 174 CTRNYIHHMLFVSFMLRATSFVKDRVVAHIGVKLESLMQDDPQNSIEATSDVKSOY 233  
Db 172 CTRNYIHHMLFVSFILRALSNFIKDAV-----LFSSDD-----VTYCD-AHK 212  
QY 234 IGCKIATVVMFYFLATNYIWLVEGLYHNLIFVAFSDTKYLVGFIIGWGFPAFVA 293  
Db 213 VGCKLVMIFFQYICINAWANLVEGLYHNLTAISFFERKYLQAFVLGWSIPAIFVAL 272  
QY 294 WAVARATLADARCWELSA-GDIKTIYQAPILAAIGLFIPLFNTVRLATKIWEYNAVGH 352  
Db 273 WAITRHLENTGCWDINANASVWVIRGPIVLSILINFIFFINILRILMKRLRTQETRGS 332  
QY 353 DTRKQYKRLAKSTLVLVLFVGVHYIVFVCLPHSFISFGWETRMHCELFNFSGQFFVSI 412  
Db 333 ET-NHYKRLAKSTLLILPFGIHYIVFAFSPED-----AMEVOLFFELALGFSQGLVAVL 387  
QY 413 YCYNGEVOAEVKKMWSRWNLSDVMKRTPPGCSRRCGSVLTTHSTSSQSO 464  
Db 388 YCFLNGEVOLEVOKKRWHLQ-EFLPRVAFNNSFNATNGPTHSTRASTE 438  
RESULT 11

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Query Match      27.0%; Score 785; DB 1; Length 458;
Best Local Similarity 37.0%; Pred. No. 2.6e-73;
Matches 182; Conservative 76; Mismatches 152; Indels 82; Gaps 18;

12 GWMLGSCLLA--RAQLSDGTITI---EEQIVLVLRKAVOCELNI-TAOLQEGNCF 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
10 GWF----CVLACVLACVLPGVSAVGLQEECDYLIQMIKVQHKOCLEAQLNETSCS 65
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
65 PEWDGLICPRGTVGKISAVPCPPYIDFN-HKVG-AFRHCNPNGTWDFMHLNKTWANY 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
66 KWNLDLTCWPAIPRGQVVVLAQPLIFKLFSPQGLNVSRRNCTDEG-----WTP- 113

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; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/437,466
; FILING DATE: 09-MAY-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-136 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: RPACAP-3/RVIP-2
; HYPOTHETICAL: NO
; US-08-538-816A-2

Query Match 24.5%; Score 713.5; DB 2; Length 437;
Best Local Similarity 33.6%; Pred. No. 6.8e-66;
Matches 163; Conservative 87; Mismatches 156; Indels 79; Gaps 15;

QY 39 VLVKAKVQCELNITAOQEGECNCP-----EWDGLICWPRGTGKISAV 84
Db 13 LLVRVSSIHPECRFHLEIOEETKCAELLSSQENQRACSGVWDNITCWRPADVGETVTV 72

QY 85 PCPPYIYDF-NHKGVAFRCHNPGNTWDFHSLNKTWANTSDCLRFQPDISIGKQFCER 143
Db 73 PCPKVFSNFSRPGNISKNTSDG-W-----SETPDFIDACGYNDPE-DESKISFYIL 124

QY 144 LYVMYTVGYSISPGSLAVAILIIGYFRRHLHCTRNYIHMHLFVSFMLRATSIYFKDRVVA 203
Db 125 VKAIYTLGYSVLSLMTTSGSIICLFKRLHCTRNYIHLNLFSLFMRALSVLKDSVLVS 184

QY 204 HIGVKELESIMODDPONSTEATSDVKQYIGCKIAVVMFIYFLATNYIWLVEGLYLNH 263
Db 185 SSGI-----LRCHDQP-----ASWVGCKLSLVFFQYCYIMANFYWLLVEGLYLHT 228

QY 264 LIFVAFSDTKYLMGFIILGWGPPAAFAVAVARATLADARCWELSAGDIK-WIYOAPI 322
Db 229 LL-VAILPPSRCLFAYLLIIGWGPSVCIGAWTATRLSLEDTGCDTNDHSIPMWVIRMPI 287

QY 323 LAAIGLNFILNTVRVLTATKIWETNAVGHDTKQYRKLAKESTLVLVVFGVHYIVFVCL 382
Db 288 LISIVNFAIFISIVRILLOKLTSPDVGND-QSQYKRLAKSTLLIPLFGVHYMVAFAF 346

QY 383 PHSETGLGWIRHCELFNFSFGFFIYCYCNCEVQAEVKMMSRNLSVDWKRTPP 442
Db 347 P-----IGISSTQILFELCVSGFGLVAVVLYCFNLSEVQCELRWR----- 390

QY 443 CGSRRCGSVLTVTHTSTSSOSVAAAHAWCLSLAKLPSPADSLTATSIYLAWSGVTSR 502
Db 391 -----GLCL-----TQAGSRDYLHWSMS-----RNGSES-----ALQIHRGSRQTQS 429

QY 503 TASHT 507
Db 430 LQSET 434
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## RESULT 15

```
US-09-076-651-2
; Sequence 2, Application US/09076651
; Patent No. 5882899
; GENERAL INFORMATION:
; APPLICANT: Mojssov, Svetlana
; APPLICANT: Wei, Yang
```

```
; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED
; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE
; THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076,651
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/538,816
; FILING DATE: 03-OCTOBER-1995
; APPLICATION NUMBER: US 08/437,466
; FILING DATE: 09-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-136 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: RPACAP-3/RVIP-2
; HYPOTHETICAL: NO
; US-09-076-651-2

Query Match 24.5%; Score 713.5; DB 2; Length 437;
Best Local Similarity 33.6%; Pred. No. 6.8e-66;
Matches 163; Conservative 87; Mismatches 156; Indels 79; Gaps 15;
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QY 39 VLVKAKVQCELNITAOQEGECNCP-----EWDGLICWPRGTGKISAV 84
Db 13 LLVRVSSIHPECRFHLEIOEETKCAELLSSQENQRACSGVWDNITCWRPADVGETVTV 72

QY 85 PCPPYIYDF-NHKGVAFRCHNPGNTWDFHSLNKTWANTSDCLRFQPDISIGKQFCER 143
Db 73 PCPKVFSNFSRPGNISKNTSDG-W-----SETPDFIDACGYNDPE-DESKISFYIL 124

QY 144 LYVMYTVGYSISPGSLAVAILIIGYFRRHLHCTRNYIHMHLFVSFMLRATSIYFKDRVVA 203
Db 125 VKAIYTLGYSVLSLMTTSGSIICLFKRLHCTRNYIHLNLFSLFMRALSVLKDSVLVS 184

QY 204 HIGVKELESIMODDPONSTEATSDVKQYIGCKIAVVMFIYFLATNYIWLVEGLYLNH 263
Db 185 SSGI-----LRCHDQP-----ASWVGCKLSLVFFQYCYIMANFYWLLVEGLYLHT 228

QY 264 LIFVAFSDTKYLMGFIILGWGPPAAFAVAVARATLADARCWELSAGDIK-WIYOAPI 322
Db 229 LL-VAILPPSRCLFAYLLIIGWGPSVCIGAWTATRLSLEDTGCDTNDHSIPMWVIRMPI 287

QY 323 LAAIGLNFILNTVRVLTATKIWETNAVGHDTKQYRKLAKESTLVLVVFGVHYIVFVCL 382
Db 288 LISIVNFAIFISIVRILLOKLTSPDVGND-QSQYKRLAKSTLLIPLFGVHYMVAFAF 346
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 21, 2001, 17:06:32 ; Search time 22.32 Seconds  
(without alignments)  
1469.426 Million cell updates/sec

Title: US-09-236-468A-2  
Perfect score: 541  
Sequence: 1 MAWLGLASLHWGWLMLGSL.....DDILMEKPSRPMESNPDTG 541

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 412676 seqs, 60623988 residues

Word size : 10  
Total number of hits satisfying chosen parameters: 49

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A\_Geneseq\_0601.\*  
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21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541	100.0	541	AAW12695	G-protein parathyroid
2	363	67.1	550	AAW17875	Human PTR2 seven t
3	262	48.4	550	AAW80560	Human PTH2 recepto
4	38	7.0	546	AAW80559	Rat PTH2 receptor
5	25	4.6	515	AAW27704	Opossum kidney PTH
6	25	4.6	515	AAW27704	Opossum kidney PTH
7	25	4.6	515	AAW27704	Parathyroid hormon
8	25	4.6	515	AAW27705	Opossum kidney PTH
9	25	4.6	585	AAW27706	Opossum kidney PTH
10	25	4.6	585	AAW73315	Parathyroid hormon
11	19	3.5	440	AAW08188	Amino acid sequenc

12	19	3.5	440	22	AAW17877	Human SCRC seven t
13	19	3.5	449	13	AAW30187	Secretin receptor.
14	18	3.3	324	21	AAW96985	Tethered PTH-1 rec
15	18	3.3	335	21	AAW96984	Tethered PTH-1 rec
16	18	3.3	435	21	AAW96987	Human tethered PTH
17	18	3.3	435	21	AAW07529	A mutant parathyro
18	18	3.3	446	21	AAW96983	Tethered PTH-1 rec
19	18	3.3	448	21	AAW96986	Human tethered PTH
20	18	3.3	450	21	AAW96988	Human tethered PTH
21	18	3.3	536	21	AAW96000	Zebrafish parathyr
22	18	3.3	536	21	AAW90230	Zebrafish PTH1R re
23	18	3.3	591	13	AAW27706	Rat bone PTH/PTHrP
24	18	3.3	591	17	AAW92277	Rat bone PTH/PTHrP
25	18	3.3	591	20	AAW73316	Parathyroid hormon
26	18	3.3	593	17	AAW92278	Human kidney PTH/p
27	18	3.3	593	20	AAW73317	Human Parathyroid
28	18	3.3	593	22	AAW71876	Human PTHrR seven t
29	18	3.3	614	13	AAW27707	Human kidney PTH/p
30	14	2.6	19	13	AAW27710	PTH/PTHrP receptor
31	14	2.6	19	17	AAW92281	PTH/PTHrP extracel
32	14	2.6	19	20	AAW73320	Parathyroid hormon
33	13	2.4	457	22	AAW71878	Human VIPR seven t
34	13	2.4	458	16	AAW72506	Porcine vasoactive
35	13	2.4	459	14	AAW42848	VIP receptor prote
36	12	2.2	445	21	AAW82704	Human glucose-depe
37	12	2.2	458	21	AAW51528	Human GIP receptor
38	12	2.2	466	21	AAW51526	Human GIP receptor
39	12	2.2	466	22	AAW71870	Human GIPR seven t
40	11	2.0	11	16	AAW70138	Opossum parathyroi
41	11	2.0	523	21	AAW90231	Zebrafish PTH3R re
42	11	2.0	542	21	AAW99601	Zebrafish parathyr
43	10	1.8	10	17	AAW92285	PTH/PTHrP intracel
44	10	1.8	162	15	AAW57829	Human GR C-termina
45	10	1.8	222	19	AAW68067	Human glucagon-lik
46	10	1.8	477	15	AAW50047	Human glucagon rec
47	10	1.8	477	22	AAW71872	Human GDR seven tr
48	10	1.8	550	19	AAW68066	Rat glucagon-like
49	10	1.8	553	19	AAW68065	Human glucagon-lik

ALIGNMENTS

RESULT 1  
AAW12695  
ID AAW12695 standard; Protein; 541 AA.  
XX  
AC AAW12695;  
XX  
DT 31-MAY-1997 (first entry)  
XX  
DE G-protein parathyroid hormone receptor HLTG74.  
XX

KW G-protein parathyroid hormone receptor; HLTG74; parathormone; PTH;  
KW calcium; signal transduction; agonist; antagonist; hypocalcaemia;  
KW hyperphosphataemia; hypoparathyroidism; chronic tetany;  
KW osteoporosis; hypercalcaemia; hypoparathyroidism; hypophosphataemia;  
KW kidney stone; nephroliasis; therapy; diagnosis.  
XX  
OS Homo sapiens.  
XX  
PN WO9639433-A1.  
XX  
PD 12-DEC-1996.  
XX  
PF 05-JUN-1995; 95WO-US07085.  
XX  
PR 05-JUN-1995; 95WO-US07085.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Li Y, Rosen CA, Ruben SM, Soppet DR;  
XX

DR WPI: 1997-043068/04.  
XX N-PSDB; AAT59619.  
XX Human G-protein parathyroid hormone receptor, HLTG74 - used to  
PT identify (ant)agonists, used in the treatment of hypo- or  
PT hyper-calcemia, hypo- or hyper-phosphatemia, kidney stones, etc  
XX  
PS Claim 9; Fig 1A-E; 62pp; English.  
XX A novel 7-transmembrane receptor (AAWL12695) has been identified as a  
CC human G-protein parathyroid hormone (PTH) receptor. designated  
CC HLTG74.. It shows 48.2% homology to the human PTH receptor. Its  
CC amino acid sequence was deduced from a cDNA clone (AAT59619) isolated  
CC from a human T cell lymphoma tissue cDNA library. Recombinant  
CC HLTG74 can be produced in transformed host cells and used to  
CC screen for (ant)agonist cpds. Agonists may be used to prevent or  
CC treat e.g. hypocalcaemia, hyperphosphataemia, hypoparathyroidism  
CC and chronic tetany by stimulating an increase in serum calcium  
CC levels. Antagonists can be used to inhibit the receptor e.g. for  
CC the treatment of osteoporosis, hypercalcaemia, hypoparathyroidism,  
CC hypophosphataemia, kidney stone, nephroliasis.  
XX Sequence 541 AA;  
SQ  
Query Match 100.0%; Score 541; DB 18; Length 541;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAWLGLSHVWGLMGLSGCLLARAQLDSGGTTTIEBQIVLVLKAKVQCELNITAQLQEGE 60  
Db 1 mawlgaslhvhwglmgslgcllaragldsgdtitieeqivlvlkakvqcelnitaqlqege 60  
QY 61 GNCFFPMDGLICWPGCTGCKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSINKTWA 120  
Db 61 gncfpwdglicwprgctgckisavpcppyiydfnhkgvafrcnpgntgdfmhsinktwa 120  
QY 121 NYSDCRLFLQDISIGKQBFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYYZH 180  
Db 121 nysdcrlflqdisigkqbfceerlymytvgyssifsgslavailiigyfrlhlctrnylh 180  
QY 181 MHLFVSFMLRATSFVKDRVVAHIGVKESLIMQDDPQNSIEATSDVKSQYIGCKIAV 240  
Db 181 mhlfsfmlratsfvdrrvvhahigvkeslimqddpqnsieatsvdksgyigckiaav 240  
QY 241 VMFIYLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFILIGWGPFAAFVAWAVARAT 300  
Db 241 vmfiylatnywylveglylnhlifvafstdtkylwgfllgwgfpafvaawavarat 300  
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTKRQYRK 360  
Db 301 ladarcwelsagdikwiyqapilaaiglnflflntvrvlatkietnavghdtrkqyrk 360  
QY 361 LAKSTLVLVFVGVHVIVFVCLPHSFSTGLGWETRMHCELFENSGQFFVSIYCYCNGEV 420  
Db 361 lakstlvlvfvgvhvfvclphsfstglgwetrmhcelfensfgqffvsiycycngev 420  
QY 421 QAEVKKMSRWNLSDVWKRTPTPCGSRRCGSLVTTVTHSTSSQVAAAHAWCLSLAKLPR 480  
Db 421 qaevkkmwswnlsvdwkrtptpcgsrrcgsvlttvthstssqvaaaahawclslaklpr 480  
QY 481 SPADSLTATSLYLSAMSGVGTQSTASHTLSTRNKEDSGRQRDILMEKPSRPMESNPDE 540  
Db 481 spadsltatslylsamsgvtqstashtlstrnkedsgqrdrdilmekpsrpmesnpdte 540  
QY 541 G 541  
Db 541 g 541  
RESULT 2  
AAB71875  
ID AAB71875 standard; Protein; 550 AA.

XX AAB71875;  
AC  
XX  
DT 03-MAY-2001 (first entry)  
DE Human PTR2 seven transmembrane domain.  
XX  
KW Human; PTR2; parathyroid hormone receptor; h15571; immunomodulatory;  
KW vascular; hepatic; antiasthma; antimicrobial; antiinflammatory;  
KW immunosuppressive; gene therapy; vaccine; G-protein coupled receptor;  
KW GPCR; liver fibrosis; respiratory disorder; infection;  
KW chronic inflammatory disease; organ-specific autoimmunity;  
KW graft rejection; cystic fibrosis.  
OS Homo sapiens.  
XX  
PN WO200109328-A1.  
XX  
PD 08-FEB-2001.  
XX  
PF 03-AUG-2000; 2000WO-US21278.  
XX  
PR 03-AUG-1999; 99US-0146916.  
PR 29-FEB-2000; 2000US-0515781.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Hodge MR, Lloyd C, Welch NS;  
XX  
DR WPI: 2001-138653/14.  
XX  
PT Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful  
PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma  
XX  
PS Disclosure: Fig 2; 145pp; English.  
XX  
CC The present sequence is a human G-protein coupled receptor (GPCR) used  
CC for comparison with the seven transmembrane domain of a novel GPCR  
CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be  
CC used in the prevention, treatment and diagnosis of diseases associated  
CC with inappropriate GPCR expression. Such diseases includes immune,  
CC haematological, fibrotic, hepatic and respiratory disorders including  
CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic  
CC infections, chronic inflammatory diseases, organ-specific autoimmunity,  
CC graft rejection, graft versus host disease, cystic fibrosis and, in  
CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens  
CC in the production of antibodies against GPCR and in assays to identify  
CC modulators (agonists and antagonists) of GPCR expression and activity.  
CC The anti-GPCR antibodies and GPCR antagonists may also be used to down  
CC regulate GPCR expression and activity. The anti-GPCR antibodies may be  
CC used as diagnostic agents for detecting the presence of GPCR  
XX polypeptides in samples.  
XX Sequence 550 AA;  
SQ  
Query Match 67.1%; Score 363; DB 22; Length 550;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 LGASLHVWGLMGLSGCLLARAQLDSGGTTTIEBQIVLVLKAKVQCELNITAQLQEGEGNC 63  
Db 4 lgaslhvhwglmgslgcllaragldsgdtitieeqivlvlkakvqcelnitaqlqegegc 63  
QY 64 FPEWDLICWPGCTGCKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSINKTWNYS 123  
Db 64 fpewdglcwprgctgckisavpcppyiydfnhkgvafrcnpgntgdfmhsinktwany 123  
QY 124 DCLRLFLQDISIGKQBFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYYHML 183  
Db 124 dclrlflqdisigkqbfceerlymytvgyssifsgslavailiigyfrlhlctrnyihml 183

QY 184 FVSPMLRATSIFFKDRVVHAIHIGVKELESIMQDDPQNSIEATSVKDSQYIGCKIAVVMF 243  
Db 184 fvsfmlratsifvkdrrvvhahigvkeleslmqddpqnsieatsvdksgyigckiaavmf 243  
QY 244 IYFLATNYWTLVSGLYLHNLIFVAFPSDTKYLNGFILIIGHGFFPAFVAANAVARATLAD 303  
Db 244 lyflatnywtlvsglylhnlifvafpsdtkylngfiliighgffpaatvaavavaratlad 303  
QY 304 ARCWELSGADIKWYIQAPILAAIGLNFILNTVRLATKIWETNAVGHDRKQYRKLA 363  
Db 304 arcwelsagdikwyiqapilaaignlfnlntvrlatkiwetnavghdrkyrklak 363  
QY 364 STLVLVLFVGHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGQFVSIYCYCNGEVOAE 423  
Db 364 stlvlvlfvghyivfvcplhspfsglglweirhmclfnfsggfvsliycycngevgae 423  
QY 424 VKMWSRWNLSDVWKRTPPCGSRRCGSLVTVTHTSTSSQSOVAA 467  
Db 424 vkwmwsrwnlsdvdkrtppcgssrrcgsvlvtvtthstssqsgvaa 467  
RESULT 3  
AAB80560  
ID AAB80560 standard; Protein: 550 AA.  
XX  
AC AAB80560;  
XX  
DT 26-APR-2001 (first entry)  
XX  
DE Human PTH2 receptor amino acid sequence.  
XX  
KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;  
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;  
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;  
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiatic;  
KW cytotatic; antiasthmatic; neuroprotective; PTH receptor antagonist;  
KW obesity; eating disorder; metabolic disorder; mental disorder;  
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;  
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;  
KW hypertension; congestive heart failure; tumour; asthma; emphysema;  
KW restrictive lung disease; demyelinating condition; multiple sclerosis;  
KW leukodystrophy.  
XX  
OS Homo sapiens.  
XX  
PN W0200077042-A2.  
XX  
PD 21-DEC-2000.  
XX  
XX 15-JUN-2000; 2000WO-US16776.  
XX  
XX 15-JUN-1999; 9905-0139335.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Usdin TB, Hoare SRJ;  
XX  
XX WPI; 2001-122833/13.  
XX  
XX New parathyroid hormone type 2 or 1 receptor ligand, useful for  
PT treating e.g. migraine or headaches, hypertension, obesity and other  
PT eating or metabolic disorders, mental disorders and osteoporosis -  
XX  
XX Example 4; Fig 1; 106pp; English.  
XX  
CC The present invention describes an isolated or purified peptide (I) that  
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1  
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,  
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,  
CC hypertensive, cardiatic, cytotatic, antiasthmatic and neuroprotective  
CC activities, and is an PTH receptor antagonist. The peptide is useful in  
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.  
CC The PTH2 receptor binding activity may be used in treating obesity or

CC other eating or metabolic disorders, mental disorders (e.g. depression,  
CC schizophrenia and dementia), acute or chronic pain, migraine or  
CC headaches, diabetes and other metabolic disorders, osteoporosis,  
CC hypercalcaemia and other disorders affecting calcium metabolism,  
CC hypertension, congestive heart failure and control of tumour growth,  
CC asthma, emphysema or other restrictive lung diseases, and demyelinating  
CC conditions such as multiple sclerosis and leukodystrophies. The present  
CC sequence represents a PTH2 receptor which is used in the  
CC exemplification of the present invention.  
XX  
XX Sequence 550 AA;  
SQ  
Query Match 48.4%; Score 262; DB 22; Length 550;  
Best Local Similarity 99.6%; Pred. No. 1e-259;  
Matches 462; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 LGASLHWGVMMLGSCLLARALQSDGTITIEQIVLVKAKVQCELNITAQLOEGEGNC 63  
Db 4 lgaslhwgvmmlgscllaraqlsdgtitieeqivlvkakvqcclnitaqlqegegnc 63  
QY 64 FPWDGLICWPRGTIVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDPHMSLNKTWANS 123  
Db 64 fpwdglicwprgtivgkisavpcppyiydfnhkgvaftrhcnpngtwdfmhslnktwans 123  
QY 124 DCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGVFRRLHCTRYIHML 183  
Db 124 dclrflopdisigkqecferlyvmytvgyisfsgslavailiigvfrlrhctryihmhl 183  
QY 184 FVSPMLRATSIFFKDRVVHAIHIGVKELESIMQDDPQNSIEATSVKDSQYIGCKIAVVMF 243  
Db 184 fvsfmlratsifvkdrrvvhahigvkeleslmqddpqnsieatsvdksgyigckiaavmf 243  
QY 244 IYFLATNYWTLVSGLYLHNLIFVAFPSDTKYLNGFILIIGHGFFPAFVAANAVARATLAD 303  
Db 244 lyflatnywtlvsglylhnlifvafpsdtkylngfiliighgffpaatvaavavaratlad 303  
QY 304 ARCWELSGADIKWYIQAPILAAIGLNFILNTVRLATKIWETNAVGHDRKQYRKLA 363  
Db 304 arcwelsagdikwyiqapilaaignlfnlntvrlatkiwetnavghdrkyrklak 363  
QY 364 STLVLVLFVGHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGQFVSIYCYCNGEVOAE 423  
Db 364 stlvlvlfvghyivfvcplhspfsglglweirhmclfnfsggfvsliycycngevgae 423  
QY 424 VKMWSRWNLSDVWKRTPPCGSRRCGSLVTVTHTSTSSQSOVAA 467  
Db 424 vkwmwsrwnlsdvdkrtppcgssrrcgsvlvtvtthstssqsgvaa 467  
RESULT 4  
AAB80559  
ID AAB80559 standard; Protein: 546 AA.  
XX  
AC AAB80559;  
XX  
DT 26-APR-2001 (first entry)  
XX  
DE Rat PTH2 receptor amino acid sequence.  
XX  
KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;  
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;  
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;  
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiatic;  
KW cytotatic; antiasthmatic; neuroprotective; PTH receptor antagonist;  
KW obesity; eating disorder; metabolic disorder; mental disorder;  
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;  
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;  
KW hypertension; congestive heart failure; tumour; asthma; emphysema;  
KW restrictive lung disease; demyelinating condition; multiple sclerosis;  
KW leukodystrophy.  
XX  
OS Rattus sp.

```
XX WO200077042-A2.
PN
XX
XX 21-DEC-2000.
PD
XX
XX 15-JUN-2000; 2000WO-US16776.
PF
XX
XX 15-JUN-1999; 99US-0193335.
PR
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
XX Usdin TB, Hoare SRJ;
PI
XX
XX WPI; 2001-122833/13.
DR
XX
XX New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
PT
XX
XX Example 4; Fig I; 106pp; English.
PS
XX
XX The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiant, cytotatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. The present
CC sequence represents a PTH2 receptor which is used in the
CC exemplification of the present invention.
XX
XX Sequence 546 AA;
SQ

Query Match 7.0%; Score 38; DB 22; Length 546;
Best Local Similarity 100.0%; Pred. No. 3.2e-30;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 WIYQAPILAAIGLNFLLFNTVRLATKIWTETNAVGH 353
DB 313 WIYQAPILAAIGLNFLLFNTVRLATKIWTETNAVGH 350

RESULT 5
AAR27704
ID AAR27704 standard; Protein; 515 AA.
XX
XX AAR27704;
AC
XX
XX 16-MAR-1993 (first entry)
DT
XX
XX Opossum kidney PTH/PTHrP receptor prep. from clone OK-H.
DE
XX
XX Parathyroid hormone; related protein; calcium; antagonist;
KW antibodies; hypercalcaemia.
XX
XX Didelphis virginiana.
OS
XX
XX WO9217602-A.
PN
XX
XX 15-OCT-1992.
PD
XX
XX 06-APR-1992; 92WO-US02821.
PF
XX
XX 05-APR-1991; 91US-0681702.
PR
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PR 06-APR-1992; 92US-0864475.
XX
XX (GEHO ) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
PA
XX
XX Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
PI Segre GV;
XX
XX WPI; 1992-366271/44.
DR
XX
XX N-PSDB; AAQ29604.
DR
XX
XX New DNA encoding parathyroid hormone receptor, DNA and antibodies
PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
PT and treatment of tumours
XX
XX Disclosure; Fig 1; 91pp; English.
PS
XX
XX The parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
CC receptor protein sequence was deduced from the DNA sequence of the
CC clone OK-H, isolated from opossum kidney (OK) cells. The protein
CC may be used in a therapeutic compsn. to inhibit activation of PTH or
CC PTHrP and thus reduce the level of calcium in the blood. Cpd.
CC capable of competing with PTH or PTHrP for binding can be identified
CC using the protein prod. and DNAs homologous to PTH DNA can be
CC identified using fragments of the clone as probes. The protein
CC may be used for the prodn. of antibodies useful for the treatment,
CC classification, prognosis and/or treatment of disorders related to
CC the interaction between a cell receptor and a ligand such as in
CC hypercalcaemia. See also AAR27705-16.
XX
XX Sequence 515 AA;
SQ

Query Match 4.6%; Score 25; DB 13; Length 515;
Best Local Similarity 100.0%; Pred. No. 6.4e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNVIHMHFVSFMLRA 191
DB 207 GYFRLHCTRNVIHMHFVSFMLRA 231

RESULT 6
AAR92275
ID AAR92275 standard; Protein; 515 AA.
XX
XX AAR92275;
AC
XX
XX 18-MAY-1996 (first entry)
DT
XX
XX Opossum kidney PTH/PTHrP receptor.
DE
XX
XX Parathyroid hormone; receptor; parathormone; PTH;
KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
KW hypercalcaemia; hypocalcaemia; cancer; opossum.
XX
XX Didelphis virginiana.
OS
XX
XX US5494806-A.
PN
XX
XX 27-FEB-1996.
PD
XX
XX 05-APR-1991; 91US-0681702.
PF
XX
XX 06-APR-1992; 92US-0864475.
PR
XX
XX 05-APR-1991; 91US-0681702.
XX
XX (GEHO ) GEN HOSPITAL CORP.
PA
XX
XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
PI Schipani E, Segre GV;
XX
XX WPI; 1996-139028/14.
DR
XX
XX N-PSDB; AAT15945.
```

XX DNA encoding vertebrate parathyroid hormone receptor - useful for  
 PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,  
 PT cancer etc.  
 XX  
 PS Claim 1; Fig 1A-1E; 64pp; English.  
 XX  
 CC Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)  
 CC receptors (AAR92275 and AAR92776) are encoded by cDNA clones OK-H  
 CC (AAT15945) and OK-O (AAT15946), respectively, isolated from an opossum  
 CC kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2  
 CC separate genes or of a laboratory artifact. The receptor induces an  
 CC increase in intracellular cAMP and calcium when challenged with PTH or  
 CC PTHrP. Recombinant receptors can be produced in vector/host cell systems  
 CC and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia  
 CC and hypocalcaemia, to screen for (ant)agonists and to raise antibodies.  
 CC Host cells expressing the receptor can be used for diagnostic  
 CC measurement of PTH serum levels.  
 XX  
 SQ Sequence 515 AA;

Query Match 4.6%; Score 25; DB 17; Length 515;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-17;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 167 GYFRRLHCTRNYYIMHFLVSPMLRA 191  
 |||||  
 Db 207 gyfrlhcetnyihmhlfsfmlra 231

RESULT 7  
 AAW73314  
 ID AAW73314 standard; Protein; 515 AA.

XX AC AAW73314;

XX DT 08-FEB-1999 (first entry)

XX DE Parathyroid hormone receptor OK-H.

XX KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;  
 XX PTH-related hypercalcaemia; opossum.

OS Didelphis virginiana.

XX PN US5840853-A.

XX PD 24-NOV-1998.

XX PF 06-JUN-1995; 95US-0471494.

XX PR 06-APR-1992; 92US-0864475.

XX PR 03-APR-1991; 91US-0681702.

XX PR 06-JUN-1995; 95US-0471494.

XX PA (GEO ) GEN HOSPITAL CORP.

XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;

XX PI Schipani E, Segre GV;

XX DR WPI; 1999-034124/03.

XX DR N-PSDB; AAV08388.

XX XX Antibody to parathyroid hormone receptor - for diagnostic or  
 PT therapeutic use

XX PS Claim 6; Fig 1; 63pp; English.

XX CC This sequence represents the opossum parathyroid hormone (PTH) receptor  
 CC OK-H, which is targeted by the antibody of the invention. The antibody  
 CC of the invention is immunoreactive with naturally occurring human, rat or  
 CC opossum PTH receptor. The antibody is useful for treating disorders

CC characterised by overstimulation of PTH receptors by their ligand and for  
 CC the diagnosis of PTH-related hypercalcaemia.  
 XX  
 SQ Sequence 515 AA;

Query Match 4.6%; Score 25; DB 20; Length 515;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-17;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLHCTRNYYIMHFLVSPMLRA 191

|||||  
 Db 207 gyfrlhcetnyihmhlfsfmlra 231

RESULT 8

AAR27705

ID AAR27705 standard; Protein; 585 AA.

XX AC AAR27705;

XX DT 16-MAR-1993 (first entry)

XX DE Opossum kidney PTH/PTHrP receptor prod. from clone OK-O.

XX KW Parathyroid hormone; related protein; calcium; antagonist;  
 KW antibodies; hypercalcaemia.

XX OS Didelphis virginiana.

XX PN WO9217602-A.

XX PD 15-OCT-1992.

XX PF 06-APR-1992; 92WO-US02821.

XX PR 05-APR-1991; 91US-0681702.

XX PR 06-APR-1992; 92US-0864475.

XX PA (GEO ) GEN HOSPITAL CORP OFFICE TECHNOLOGY.

XX PI Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;  
 XX PI Segre GV;

XX DR WPI; 1992-366271/44.

XX DR N-PSDB; AAQ29605.

XX PT New DNA encoding parathyroid hormone receptor, DNA and antibodies  
 XX - for (differential) diagnosis of hypercalcaemia, and diagnosis  
 XX and treatment of tumours

XX PS Disclosure; Fig 2; 91pp; English.

XX CC The parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)  
 CC receptor protein sequence was deduced from the DNA sequence of the  
 CC clone OK-O, isolated from opossum kidney (OK) cells. The clone OK-O  
 CC is identical to the OK-H clone except at the C-terminal tail as OK-O  
 CC encodes a 585 amino acid protein, OK-H encodes one of 515 amino acids.  
 CC The difference is attributed to a single nucleotide deleted in the OK-H  
 CC sequence causing a frame shift and an earlier stop codon. It is not  
 CC known whether OK-O and OK-H represent prods. of two separate genes or  
 CC a laboratory artifact. The protein may be used in a therapeutic  
 CC compsn. to inhibit activation of PTH or PTHrP and thus reduce the  
 CC level of calcium in the blood. Cpts. capable of competing with PTH  
 CC or PTHrP for binding can be identified using the protein prod. and  
 CC DNAs homologous to PTH DNA can be identified using fragments of the  
 CC clone as probes. The sequence may be used for the prodn. of antibodies  
 CC useful for the treatment, classification, prognosis and/or treatment of  
 CC disorders related to the interaction between a cell receptor and a  
 CC ligand such as in hypercalcaemia. See also AAR27704-16.

XX SQ Sequence 585 AA;

```
Query Match      4.6%; Score 25; DB 13; Length 585;
Best Local Similarity 100.0%; Pred. No. 7.1e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNVIHMHFLVFSFMLRA 191
    |||||||
Db 207 gyfrrlhcrtynyhmhlfvsmfmlra 231

RESULT 9
AAR92276
ID AAR92276 standard; Protein; 585 AA.
XX AC AAR92276;
XX XX 18-MAY-1996 (first entry)
XX DE Opossum kidney PTH/PTHrP receptor.
XX KW Parathyroid hormone; receptor; parathormone; PTH;
XX KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
XX KW hypercalcaemia; hypocalcaemia; cancer; opossum.
XX OS Didelphis virginiana.
XX XX US5494806-A.
XX PN 27-FEB-1996.
XX PD 05-APR-1991; 91US-0681702.
XX PF 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX XX (GEO ) GEN HOSPITAL CORP.
XX PA Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
XX PI Schipani E, Segre GV;
XX XX WPI; 1996-139028/14.
XX DR N-PSDB; AAT15946.
XX XX DNA encoding vertebrate parathyroid hormone receptor - useful for
XX PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
XX PT cancer etc.
XX PS Claim 1; Fig 2A-2E; 64pp; English.
XX XX Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
XX CC receptors (AAR92275 and AAR92276) are encoded by cDNA clones OK-H
XX CC (AAT15945) and OK-O (AAT15946), respectively, isolated from an opossum
XX CC kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2
XX CC separate genes or of a laboratory artifact. The receptor induces an
XX CC increase in intracellular cAMP and calcium when challenged with PTH or
XX CC PTHrP. Recombinant receptors can be produced in vector/host cell systems
XX CC and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia
XX CC and hypocalcaemia, to screen for (ant)agonists and to raise antibodies.
XX CC Host cells expressing the receptor can be used for diagnostic
XX CC measurement of PTH serum levels.
XX XX Sequence 585 AA;

Query Match      4.6%; Score 25; DB 17; Length 585;
Best Local Similarity 100.0%; Pred. No. 7.1e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNVIHMHFLVFSFMLRA 191
    |||||||
Db 207 gyfrrlhcrtynyhmhlfvsmfmlra 231

RESULT 10
AAW73315
ID AAW73315 standard; Protein; 585 AA.
XX AC AAW73315;
XX XX 08-FEB-1999 (first entry)
XX DE Parathyroid hormone receptor OK-O.
XX KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
XX KW PTH-related hypercalcaemia; opossum.
XX OS Didelphis virginiana.
XX XX US5840853-A.
XX PN 24-NOV-1998.
XX PD 06-JUN-1995; 95US-0471494.
XX PF 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX PR 06-JUN-1995; 95US-0471494.
XX XX (GEO ) GEN HOSPITAL CORP.
XX PA Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
XX PI Schipani E, Segre GV;
XX XX WPI; 1999-034124/03.
XX DR N-PSDB; AAV08389.
XX XX Antibody to parathyroid hormone receptor - for diagnostic or
XX PT therapeutic use
XX PT Claim 6; Fig 2; 63pp; English.
XX XX This sequence represents the opossum parathyroid hormone (PTH) receptor
XX CC OK-O, which is targeted by the antibody of the invention. The antibody
XX CC of the invention is immunoreactive with naturally occurring human, rat or
XX CC opossum PTH receptor. The antibody is useful for treating disorders
XX CC characterised by overstimulation of PTH receptors by their ligand and for
XX CC the diagnosis of PTH-related hypercalcaemia.
XX XX Sequence 585 AA;

Query Match      4.6%; Score 25; DB 20; Length 585;
Best Local Similarity 100.0%; Pred. No. 7.1e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNVIHMHFLVFSFMLRA 191
    |||||||
Db 207 gyfrrlhcrtynyhmhlfvsmfmlra 231

RESULT 11
AAB08188
ID AAB08188 standard; Protein; 440 AA.
XX AC AAB08188;
XX XX 04-DEC-2000 (first entry)
XX DE Amino acid sequence of rat secretin receptor polypeptide.
XX KW Secretin; gastrointestinal hormone; pancreatic fluid; S cell;
XX KW pancreatic cell growth; pancreatic beta cell; pancreatic islet;
XX KW insulin production; glucose metabolism; insulin resistance;
XX KW glucose intolerance; hyperglycemia; hyperinsulinemia; obesity;
XX KW hyperlipidemia; hyperproteinemia; Type II diabetes mellitus;
XX KW secretin receptor.
```

XX OS Rattus sp.  
XX PN WO200047721-A2.  
XX PD 17-AUG-2000.  
XX PF 10-FEB-2000; 2000WO-US03422.  
XX PR 10-FEB-1999; 99US-0119575.  
XX PA (ONTO-) ONTOGENY INC.  
XX PI Kagan D, Pang K;  
XX DR WPI; 2000-515058/46.  
XX DR N-PSDB; AAA63813.  
XX PT Secretin therapeutic is used to modulate the growth state of pancreatic  
PT cells to provide treatment for diabetes through modification of glucose  
PT metabolism -  
XX PS Disclosure; Page 88-90; 90pp; English.  
XX CC The present sequence represents a rat secretin receptor polypeptide.  
CC Secretin is a gastrointestinal hormone that stimulates the secretion of  
CC bicarbonate-rich pancreatic fluid. Secretin is produced by specific  
CC endocrine cells (S cells) located in the mucosa of the proximal small  
CC intestine. Secretion of secretin is stimulated by the presence of either  
CC acidic pH or fatty acids in the duodenum. The specification describes  
CC a method for modulating the growth state of pancreatic cells. The method  
CC comprises contacting the cells with a secretin therapeutic or prodrug  
CC form of secretin. Secretin is used to modulate the growth state of  
CC pancreatic cells, in particular to promote the proliferation of  
CC pancreatic cells, generate functional pancreatic beta cells from  
CC pancreatic islets or cells, promote insulin production in a pancreatic  
CC islet or cell, antagonize insulin inhibition of secretin response in  
CC secretin-responsive cells, modify glucose metabolism in an animal to  
CC treat a disease associated with altered glucose metabolism e.g. insulin  
CC resistance, glucose intolerance or non-responsiveness, hyperglycemia,  
CC hyperinsulinemia, obesity, hyperlipidemia, hyperproteinemia or Type II  
CC diabetes mellitus (NIDDM).  
XX SQ Sequence 440 AA;  
  
Query Match 3.5%; Score 19; DB 21; Length 440;  
Best Local Similarity 100.0%; Pred. No. 7.8e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 169 FRLHCTRNTHMHLFVSF 187  
Db 167 frrlhctrnthmhlfsf 185  
|||||  
RESULT 12  
AAB71877  
ID AAB71877 standard; Protein; 440 AA.  
XX AC AAB71877;  
XX DT 03-MAY-2001 (first entry)  
XX OS Human SCRC seven transmembrane domain.  
XX DE Human; SCRC; secretin receptor; h15571; immunomodulatory; vascular;  
KW hepatic; antiasthma; antimicrobial; antiinflammatory; immunosuppressive;  
KW gene therapy; vaccine; G-protein coupled receptor; GPCR; liver fibrosis;  
KW respiratory disorder; infection; chronic inflammatory disease;  
KW organ-specific autoimmunity; graft rejection; cystic fibrosis.  
XX OS Homo sapiens.  
XX

PN WO200109328-A1.  
XX PD 08-FEB-2001.  
XX PF 03-AUG-2000; 2000WO-US21278.  
XX PR 03-AUG-1999; 99US-0146916.  
XX PR 29-FEB-2000; 2000US-0515781.  
XX PA (MILL-) MILLENNIUM PHARM INC.  
XX PI Hodge MR, Lloyd C, Welch NS;  
XX DR WPI; 2001-138653/14.  
XX PT Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful  
PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma  
PT -  
XX PS Disclosure; Fig 2; 145pp; English.  
XX CC The present sequence is a human G-protein coupled receptor (GPCR) used  
CC for comparison with the seven transmembrane domain of a novel GPCR  
CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be  
CC used in the prevention, treatment and diagnosis of diseases associated  
CC with inappropriate GPCR expression. Such diseases includes immune,  
CC haematological, fibrotic, hepatic and respiratory disorders including  
CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic  
CC infections, chronic inflammatory diseases, organ-specific autoimmunity,  
CC graft rejection, graft versus host disease, cystic fibrosis and, in  
CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens  
CC in the production of antibodies against GPCR and in assays to identify  
CC modulators (agonists and antagonists) of GPCR expression and activity.  
CC The anti-GPCR antibodies and GPCR antagonists may also be used to down  
CC regulate GPCR expression and activity. The anti-GPCR antibodies may be  
CC used as diagnostic agents for detecting the presence of GPCR  
CC polypeptides in samples.  
XX SQ Sequence 440 AA;  
  
Query Match 3.5%; Score 19; DB 22; Length 440;  
Best Local Similarity 100.0%; Pred. No. 7.8e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 169 FRLHCTRNTHMHLFVSF 187  
Db 167 frrlhctrnthmhlfsf 185  
|||||  
RESULT 13  
AAR30187  
ID AAR30187 standard; Protein; 449 AA.  
XX AC AAR30187;  
XX DT 28-APR-1993 (first entry)  
XX DE Secretin receptor.  
XX KW Rat; rat/mouse hybridoma; NG 108-15.  
XX OS Rattus rattus.  
XX FH Key Location/Qualifiers  
FT Peptide 1..22 /note= "signal peptide"  
FT Protein 23..449 /note= "mature secretin receptor"  
FT Modified-site 72 /note= "potential N-glycosylation site"  
FT Modified-site 100 /note= "potential N-glycosylation site"  
FT

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FT Modified-site 106 /note= "potential N-glycosylation site"
FT Modified-site 128 /note= "potential N-glycosylation site"
FT Modified-site 291 /note= "potential N-glycosylation site"
FT Domain 144..165 /note= "transmembrane domain"
FT Domain 175..194 /note= "transmembrane domain"
FT Domain 217..240 /note= "transmembrane domain"
FT Domain 254..276 /note= "transmembrane domain"
FT Domain 294..317 /note= "transmembrane domain"
FT Domain 343..362 /note= "transmembrane domain"
FT Domain 374..394 /note= "transmembrane domain"
XX WO9221754-A.
XX PN
XX XX
XX PD 10-DEC-1992.
XX PF 05-JUN-1992; 92WO-JP00728.
XX PR 07-JUN-1991; 91JP-0163946.
XX PA (OSAB-) OSAKA BIOSCIENCE INST.
XX PI Ishihara T, Nagata S, Takahashi K;
XX DR
XX DR WPI: 1992-433652/52.
XX DR N-PSDB; AAQ33018.
XX XX
XX PT DNA coding for secretin receptor - is expressed in COS cells and
XX produces a receptor protein for research and clinical use
XX PT
XX PS Claim 2; Fig 1; 44pp; Japanese.
XX CC The secretin receptor was encoded by a DNA sequence of rat origin,
XX contained in rat/mouse hybridoma NG108-15. The DNA sequence was
XX obtd. from a cDNA library derived from NG108-15 cells. Expression
XX in a suitable host allows prodn. of the receptor protein. The
XX secretin receptor protein encoded by this gene may be used in basic
XX research and in clinical tests, and is available in high yield.
XX SQ Sequence 449 AA;

Query Match 3.5%; Score 19; DB 13; Length 449;
Best Local Similarity 100.0%; Pred. No. 7.9e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNRYIHMHLFVSF 187
Db 167 frrlhctrnryihmhlfsf 185
|||||
|||||

RESULT 14
AAY96985
ID AAY96985 standard; Protein; 324 AA.
XX AC
XX AAY96985;
XX XX
XX DT 19-DEC-2000 (first entry)
XX DE Tethered PTH-1 receptor, r-del-Nt/Ct.
XX KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
XX PTH-1 receptor; resorption; remodeling; r-delta-Nt/Ct;
XX KW tethered receptor; osteoporosis.
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```
XX OS Chimeric - Rattus sp.
XX OS Synthetic.
XX PN WO200039278-A2.
XX PD 06-JUL-2000.
XX PF 30-DEC-1999; 99WO-US31108.
XX PR 31-DEC-1998; 98US-0114577.
XX PA (GARD/) GARDELLA T J.
XX PA (KRON/) KRONENBERG H M.
XX PA (POTT/) POTTS J T.
XX PA (JUEP/) JUEPPNER H.
XX PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX DR WPI: 2000-452384/39.
XX DR N-PSDB; AAA51734.
XX XX
XX PT New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass
XX Claim 22; Fig 10; 119pp; English.
XX CC Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or
XX S-(L)_n-R, are new. S is an amino terminal signaling functional domain
XX of parathyroid hormone (PTH); L is a linker molecule present n times
XX (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
XX binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
XX R_1 is the PTH-1 receptor signal sequence; and R is a portion of PTH-1
XX receptor sequence. The new compounds are used for treating mammalian
XX conditions characterized by decreases in bone mass, determining rates of
XX bone reformation, bone resorption and/or bone remodeling, treating
XX diseases and disorders associated with decreased tethelr activity,
XX increasing CAMP in a mammalian cell having PTH-1 receptors, or screening
XX for a peptide or non-peptide PTH (claimed). The new compound can be
XX administered by inhalation unlike the large native PTH or PTHrP which
XX avoids the need for regular injections to treat osteoporosis.
XX SQ Sequence 324 AA;

Query Match 3.3%; Score 18; DB 21; Length 324;
Best Local Similarity 100.0%; Pred. No. 6.2e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
Db 134 yflatnywilverglylh 151
|||||
|||||

RESULT 15
AAY96984
ID AAY96984 standard; Protein; 335 AA.
XX AC
XX AAY96984;
XX XX
XX DT 31-OCT-2000 (first entry)
XX DE Tethered PTH-1 receptor, TetherlC.
XX KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
XX PTH-1 receptor; resorption; remodeling; tetheric; osteoporosis.
XX OS Chimeric - Rattus sp.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..23
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FT Peptide /label= PTH-1_receptor_signal_sequence
FT 24..32
FT /label= PTH_residues_1-9
FT Peptide 33..36
FT /label= linker
FT Protein 37..335
FT /label= PTH-1_receptor
FT /note= "residue 182 to 480"
XX WO200039278-A2.
XX
XX PD 06-JUL-2000.
XX
XX PF 30-DEC-1999; 99WO-US31108.
XX
XX PR 31-DEC-1998; 98US-0114577.
XX
XX PA (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX
XX PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
XX DR WPI; 2000-452384/39.
XX N-PSDB; AAA51733.
XX
XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass
XX
XX PS Claim 22; Fig 9; 119pp; English.
XX
XX Compounds of the structure or formula S-(L)n-B, R1-S-(L)n-R or
XX S-(L)n-R, are new. S is an amino terminal signaling functional domain
XX of parathyroid hormone (PTH); L is a linker molecule present n times
XX (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
XX binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
XX R1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
XX receptor sequence. The new compounds are used for treating mammalian
XX conditions characterized by decreases in bone mass, determining rates of
XX bone reformation, bone resorption and/or bone remodeling, treating
XX diseases and disorders associated with decreased tetherl activity,
XX increasing cAMP in a mammalian cell having PTH-1 receptors, or screening
XX for a peptide or non-peptide PTH (claimed). The new compound can be
XX administered by inhalation unlike the large native PTH or PTHrp which
XX avoids the need for regular injections to treat osteoporosis.
XX
XX SQ Sequence 335 AA;
XX
XX Query Match 3.3%; Score 18; DB 21; Length 335;
XX Best Local Similarity 100.0%; Pred. No. 6.4e-10;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 245 YFLATNYWILVEGLYLH 262
XX |||||||||||||||
XX Db 145 yflatnywilverglylh 162
XX
XX RESULT 16
XX AAY96987
XX ID AAY96987 standard; Protein; 435 AA.
XX
XX AC AAY96987;
XX
XX DT 31-OCT-2000 (first entry)
XX
XX DE Human tethered PTH-1 receptor, hdelNT.
XX
XX KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
XX PTH-1 receptor; resorption; remodeling; tetherl; osteoporosis.
XX
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```
OS Chimeric - Homo sapiens.
OS Synthetic.
XX
XX PN WO200039278-A2.
XX
XX PD 06-JUL-2000.
XX
XX PF 30-DEC-1999; 99WO-US31108.
XX
XX PR 31-DEC-1998; 98US-0114577.
XX
XX PA (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX
XX PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
XX DR WPI; 2000-452384/39.
XX N-PSDB; AAA51736.
XX
XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass
XX
XX PS Example 4; Fig 18; 119pp; English.
XX
XX Compounds of the structure or formula S-(L)n-B, R1-S-(L)n-R or
XX S-(L)n-R, are new. S is an amino terminal signaling functional domain
XX of parathyroid hormone (PTH); L is a linker molecule present n times
XX (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
XX binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
XX R1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
XX receptor sequence. The new compounds are used for treating mammalian
XX conditions characterized by decreases in bone mass, determining rates of
XX bone reformation, bone resorption and/or bone remodeling, treating
XX diseases and disorders associated with decreased tetherl activity,
XX increasing cAMP in a mammalian cell having PTH-1 receptors, or screening
XX for a peptide or non-peptide PTH (claimed). The new compound can be
XX administered by inhalation unlike the large native PTH or PTHrp which
XX avoids the need for regular injections to treat osteoporosis.
XX
XX SQ Sequence 435 AA;
XX
XX Query Match 3.3%; Score 18; DB 21; Length 435;
XX Best Local Similarity 100.0%; Pred. No. 8.1e-10;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 245 YFLATNYWILVEGLYLH 262
XX |||||||||||||||
XX Db 132 yflatnywilverglylh 149
XX
XX RESULT 17
XX AAB07529
XX ID AAB07529 standard; Protein; 435 AA.
XX
XX AC AAB07529;
XX
XX DT 20-OCT-2000 (first entry)
XX
XX DE A mutant parathyroid hormone (PTH) receptor designated rdeltant.
XX
XX KW Mutant; parathyroid hormone; PTH; receptor; rdeltant;
XX ligand binding domain.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..22 /note= "signal peptide"
XX FT Protein 23..435
```

```
FT XX /note= "mature protein"
PN XX WO200040698-A1.
XX PD 13-JUL-2000.
XX PF 31-DEC-1998; 98WO-US27862.
XX PR 31-DEC-1998; 98WO-US27862.
XX PA (GEHO ) GEN HOSPITAL CORP.
XX PI Gardella TJ, Kronenberg HM, Potts JT;
XX DR WPI: 2000-465971/40.
XX DR N-PSDB; AAA58932.
XX PT New parathyroid hormone (PTH) receptor, r-delta-Nt, characterized by a
PT deletion of the extracellular amino-terminus ligand binding domain,
PT useful in screening assays for identifying agonists and antagonists of
PT PTH receptor activity
XX PS Claim 17; Fig 1; 81pp; English.
XX CC The present sequence represents a mutant parathyroid hormone (PTH)
CC receptor, designated rdelta. The polypeptide is characterised
CC by a deletion of the extracellular amino-terminus ligand binding
CC domain. The receptor has a minimal domain for ligand binding and
CC is, therefore, useful in screening assays designed for the
CC identification of agonists and antagonists of PTH receptor
CC activity.
XX SQ Sequence 435 AA;

Query Match 3.3%; Score 18; DB 21; Length 435;
Best Local Similarity 100.0%; Pred. No. 8.1e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWYWLVEGLYLH 262
DB 134 YFLATNYWYWLVEGLYLH 151

RESULT 18
AAY96983
ID AAY96983 standard; Protein; 446 AA.
XX AC AAY96983;
XX DT 31-OCT-2000 (first entry)
XX DE Tethered PTH-1 receptor, Tether1.
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.
XX OS Chimeric - Rattus sp.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Peptide 1..23
FT Peptide /label= PTH-1_receptor_signal_sequence
FT Peptide 24..32
FT Peptide /label= PTH_residues_1-9
FT Peptide 33..36
FT Peptide /label= linker
FT Protein 37..446
FT /label= PTH-1_receptor
FT /note= "residue 182 to end"
XX WO200039278-A2.
XX
```

```
PD 06-JUL-2000.
XX 30-DEC-1999; 99WO-US31108.
XX PR 31-DEC-1998; 98US-0114577.
XX (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX DR WPI: 2000-452384/39.
XX DR N-PSDB; AAA51732.
XX PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass
XX Claim 22; Fig 7; 119pp; English.
XX CC Compounds of the structure or formula S-(L)n-B, R1-S-(L)n-R or
CC S-(L)n-R, are new. S is an amino terminal signaling functional domain
CC of parathyroid hormone (PTH); L is a linker molecule present n times
CC (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
CC binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
CC R1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
CC receptor sequence. The new compounds are used for treating mammalian
CC conditions characterized by decreases in bone mass, determining rates of
CC bone reformation, bone resorption and/or bone remodeling, treating
CC diseases and disorders associated with decreased tether1 activity,
CC increasing CAMP in a mammalian cell having PTH-1 receptors, or screening
CC for a peptide or non-peptide PTH (claimed). The new compound can be
CC administered by inhalation unlike the large native PTH or PTHrp which
CC avoids the need for regular injections to treat osteoporosis.
XX SQ Sequence 446 AA;

Query Match 3.3%; Score 18; DB 21; Length 446;
Best Local Similarity 100.0%; Pred. No. 8.3e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWYWLVEGLYLH 262
DB 145 YFLATNYWYWLVEGLYLH 162

RESULT 19
AAY96986
ID AAY96986 standard; Protein; 448 AA.
XX AC AAY96986;
XX DT 31-OCT-2000 (first entry)
XX DE Human tethered PTH-1 receptor, Tether1.
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis; ss.
XX OS Chimeric - Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Peptide 1..23
FT Peptide /label= Signal_sequence
FT Peptide /note= "Human PTH-1 receptor residues 1-23"
FT Peptide 24..32
FT Peptide /label= PTH(1-9)
FT Peptide 33..36
FT Peptide /label= Linker
```

```
FT Protein 37..448 /label= PTH-1_receptor
FT /note= "Human PTH-1 receptor residues 182-593"
XX WO200039278-A2.
XX 06-JUL-2000.
XX 30-DEC-1999; 99WO-US311108.
XX 31-DEC-1998; 98US-0114577.
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-452384/39.
XX N-PSDB; AAA51735.
XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass
XX Example 4; Fig 17; 119pp; English.
XX Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or
XX S-(L)_n-R, are new. S is an amino terminal signaling functional domain
XX of parathyroid hormone (PTH); L is a linker molecule present n times
XX (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
XX binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
XX R_1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
XX receptor sequence. The new compounds are used for treating mammalian
XX conditions characterized by decreases in bone mass, determining rates of
XX bone reformation, bone resorption and/or bone remodeling, treating
XX diseases and disorders associated with decreased tether1 activity,
XX increasing cAMP in a mammalian cell having PTH-1 receptors, or screening
XX for a peptide or non-peptide PTH (claimed). The new compound can be
XX administered by inhalation unlike the large native PTH or PTHrP which
XX avoids the need for regular injections to treat osteoporosis.
XX Sequence 448 AA;
Query Match 3.3%; Score 18; DB 21; Length 448;
Best Local Similarity 100.0%; Pred. No. 8.3e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 YFLATNYWILVEGLYLH 262
DB 145 yflatnywilverglylh 162
RESULT 20
AAY96988
ID AAY96988 standard; Protein; 450 AA.
XX AAY96988;
XX 31-OCT-2000 (first entry)
XX Human tethered PTH-1 receptor, Tether-R11.
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
XX PTH-1 receptor; resorption; remodeling; tether-R11; osteoporosis; ss.
XX Chimeric - Homo sapiens.
XX Synthetic.
XX Key Location/Qualifiers
FT Peptide 1..23
```

```
FT /label= Signal_sequence
FT /note= "Human PTH-1 receptor residues 1-23"
XX 24..34
XX /label= PTH(1-11)
XX 35..38
XX /label= Linker
XX 39..450
XX /label= PTH-1_receptor
XX /note= "Human PTH-1 receptor residues 182-593"
XX WO200039278-A2.
XX 06-JUL-2000.
XX 30-DEC-1999; 99WO-US311108.
XX 31-DEC-1998; 98US-0114577.
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-452384/39.
XX N-PSDB; AAA51737.
XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass
XX Example 4; Fig 19; 119pp; English.
XX Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or
XX S-(L)_n-R, are new. S is an amino terminal signaling functional domain
XX of parathyroid hormone (PTH); L is a linker molecule present n times
XX (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
XX binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
XX R_1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
XX receptor sequence. The new compounds are used for treating mammalian
XX conditions characterized by decreases in bone mass, determining rates of
XX bone reformation, bone resorption and/or bone remodeling, treating
XX diseases and disorders associated with decreased tether1 activity,
XX increasing cAMP in a mammalian cell having PTH-1 receptors, or screening
XX for a peptide or non-peptide PTH (claimed). The new compound can be
XX administered by inhalation unlike the large native PTH or PTHrP which
XX avoids the need for regular injections to treat osteoporosis.
XX Sequence 450 AA;
Query Match 3.3%; Score 18; DB 21; Length 450;
Best Local Similarity 100.0%; Pred. No. 8.4e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 YFLATNYWILVEGLYLH 262
DB 147 yflatnywilverglylh 164
RESULT 21.
AAY99600
ID AAY99600 standard; Protein; 536 AA.
XX AAY99600;
XX 27-OCT-2000 (first entry)
XX Zebrafish parathyroid hormone type-1 receptor PTH1R.
XX Zebrafish; parathyroid hormone type-1 receptor; PTH1R;
XX developmental disorder; physiological disorder; neurological disorder.
KW
```

XX OS Brachydanio rerio.  
 XX XX WO200032775-A1.  
 XX PD 08-JUN-2000.  
 XX XX 30-NOV-1999; 99WO-US28207.  
 XX PF 30-NOV-1999; 98US-0110467.  
 XX PR (JUEP/) JUEPPNER H.  
 XX PA (RUBI/) RUBIN D A.  
 XX PI Jueppner H, Rubin DA;  
 XX XX WPI: 2000-412323/35.  
 DR N-PSDB; AAA49625.  
 XX XX New nucleic acids encoding parathyroid hormone receptors PTH1R and PTH3R, useful for treating diseases or disorders associated with impaired receptor functions comprises a specific nucleotide sequence -  
 XX PT Claim 17; Fig 2A; 11lpp; English.  
 XX CC The present sequence is the parathyroid hormone type-1 receptor (PTH1R) from the zebrafish. Its coding sequence was obtained by sequencing a cDNA clone. The gene and protein can be used to detect diseases in man where the receptor is either overexpressed or underexpressed, and they can be used to treat these diseases, which may be developmental, physiological or neurological disorders. They can also be used to identify agonists and antagonists which can be used in a similar manner. In addition, the gene can be used for chromosome identification.  
 XX CC Sequence 536 AA;  
 SQ  
 Query Match 3.3%; Score 18; DB 21; Length 536;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 167 GYFRLHCTRNVIHMLF 184  
 Db 167 gyfrrlhctrnyihmlf 184  
 RESULT 22  
 AAY90230  
 ID AAY90230 standard; Protein; 536 AA.  
 XX AC  
 XX AC AAY90230;  
 XX DT 29-AUG-2000 (first entry)  
 XX DE Zebrafish PTH1R receptor protein sequence.  
 XX KW Zebrafish; PTH1R receptor; PTH3R receptor; diagnosis; cancer;  
 KW parathyroid hormone type 1 receptor; parathyroid hormone type 3 receptor.  
 XX OS Brachydanio rerio.  
 XX PN WO200032771-A1.  
 XX XX 08-JUN-2000.  
 XX PD 28-MAY-1999; 99WO-US11883.  
 XX PF 30-NOV-1998; 98US-0110467.  
 XX PR (JUEP/) JUEPPNER H.  
 XX PA (RUBI/) RUBIN D A.  
 XX PI

PI Jueppner H, Rubin DA;  
 XX WPI: 2000-412319/35.  
 DR N-PSDB; AAA30828.  
 XX PT Novel zebrafish parathyroid hormone/parathyroid hormone related peptide receptor 3 and isolated nucleic acid encoding zebrafish parathyroid hormone receptor 1 for treating disorders associated with receptor function -  
 XX PT Claim 17; Fig 2a; 11lpp; English.  
 XX CC This sequence is a parathyroid hormone receptor type 1 (PTH1R) receptor protein of the invention. The invention also relates to a PTH3R receptor protein. Antagonists of PTH1R or PTH3R can be used for the treatment of diseases associated with an increase in PTH1R or PTH3R activity, respectively. The peptides are used for diagnosis or prognosis of diseases and disorders associated with PTH3R or PTH1R, such as cancer. The polypeptides can be used as a molecular weight markers on sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) gels, or on molecular sieve gel filtration columns. Antigenic epitope-bearing peptides and polypeptides are useful to raise antibodies, including monoclonal antibodies, that bind specifically to a polypeptide. The peptides are useful during diagnosis of diseases and disorders in mammals involving PTH1R or PTH3R receptor expression or function. Mutations that affect PTH1R or PTH3R sequence and/or expression levels of PTH1R or PTH3R could be diagnostic for patients with disease or disorders of a developmental, physiological or neurological nature. The nucleic acid molecules are valuable for chromosome identification. The mapping of DNAs to chromosomes is an important first step in correlating those sequences with genes associated with disease.  
 XX CC Sequence 536 AA;  
 SQ  
 Query Match 3.3%; Score 18; DB 21; Length 536;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 167 GYFRLHCTRNVIHMLF 184  
 Db 167 gyfrrlhctrnyihmlf 184  
 RESULT 23  
 AAR27706  
 ID AAR27706 standard; Protein; 591 AA.  
 XX AC  
 XX AC AAR27706;  
 XX DT 16-MAR-1993 (first entry)  
 XX DE Rat bone PTH/PTHrP receptor clone R15B prod.  
 XX KW Parathyroid hormone; related protein; calcium; antagonist;  
 KW antibodies; hypercalcaemia.  
 XX OS Rattus rattus.  
 XX PN WO9217602-A.  
 XX XX 15-OCT-1992.  
 XX PD 06-APR-1992; 92WO-US02821.  
 XX PF 05-APR-1991; 91US-0681702.  
 PR 06-APR-1992; 92US-0864475.  
 XX (GEO ) GEN HOSPITAL CORP OFFICE TECHNOLOGY.  
 XX PA Abou-samra A, Jueppner H, Kronenberg HM, Potts JT, Schipani E;  
 PI Segre GV;  
 XX PI

DR WPI; 1992-366271/44.  
 XX N-PSDB; AAR29606.  
 CC  
 CC New DNA encoding parathyroid hormone receptor, DNA and antibodies  
 PT - for (differential) diagnosis of hypercalcaemia, and diagnosis  
 PT and treatment of tumours  
 XX  
 PS Claim 20; Fig 3; 91pp; English.  
 XX  
 CC The rat bone parathyroid hormone/parathyroid hormone related  
 CC protein (PTH/PTHrP) receptor protein sequence was deduced from  
 CC clone R15B obtd. by screening a rat osteosarcoma (ROS) cell cDNA library  
 CC to isolate those expressing functionally intact PTH/PTHrP receptor  
 CC proteins, performed according to Gearing et al., (EMBO J. 8: 3676,  
 CC 1989), by identifying colonies capable of binding a suitable radio-  
 CC labelled ligand. The protein may be used in a therapeutic compsn. to  
 CC inhibit activation of PTH or PTHrP and thus reduce the level of calcium  
 CC in the blood. Cpds. capable of competing with PTH or PTHrP for binding  
 CC can be identified using the protein and DNAs homologous to PTH DNA can  
 CC be identified using fragments of the clone as probes. The sequence  
 CC may be used for the prodn. of antibodies useful for the treatment,  
 CC classification, prognosis and/or treatment of disorders related to  
 CC the interaction between a cell receptor and a ligand such as in  
 CC hypercalcaemia. See also AAR27704-16.  
 XX  
 SQ Sequence 591 AA;

Query Match 3.3%; Score 18; DB 13; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYH 262  
 |||||  
 Db 290 yflatnywilverglyh 307

RESULT 24  
 AAR92277  
 ID AAR92277 standard; Protein; 591 AA.  
 AC AAR92277;  
 XX  
 XX 18-MAY-1996 (first entry)  
 XX  
 XX Rat bone PTH/PTHrP receptor.  
 XX  
 KW Parathyroid hormone; receptor; parathormone; PTH;  
 KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;  
 KW hypercalcaemia; hypocalcaemia; cancer.  
 XX  
 OS Rattus sp.

Key Location/Qualifiers  
 FT Region 1..192  
 FT /label= Extracellular\_region  
 FT 193..211  
 FT /label= Transmembrane\_region  
 FT 212..221  
 FT /label= Intracellular\_region  
 FT 222..240  
 FT /label= Transmembrane\_region  
 FT 241..299  
 FT /label= Extracellular\_region  
 FT 300..316  
 FT /label= Transmembrane\_region  
 FT 317..325  
 FT /label= Intracellular\_region  
 FT 326..342  
 FT /label= Transmembrane\_region  
 FT 343..364  
 FT /label= Extracellular\_region  
 FT 365..383

FT Region /label= Transmembrane\_region  
 FT 384..408  
 FT /label= Intracellular\_region  
 FT 409..428  
 FT /label= Transmembrane\_region  
 FT 429..444  
 FT /label= Intracellular\_region  
 FT 445..463  
 FT /label= Transmembrane\_region  
 FT 464..591  
 FT /label= Intracellular\_region  
 XX  
 PN US5494806-A.  
 XX  
 PD 27-FEB-1996.  
 XX  
 XX 05-APR-1991; 91US-0681702.  
 PF  
 XX 06-APR-1992; 92US-0864475.  
 PR  
 PR 05-APR-1991; 91US-0681702.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 XX  
 XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;  
 PI Schipani E, Segre GV;  
 PI  
 XX WPI: 1996-139028/14.  
 DR N-PSDB; AAT15947.  
 XX  
 XX DNA encoding vertebrate parathyroid hormone receptor - useful for  
 PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,  
 PT cancer etc.  
 PT  
 XX Claim 1; Fig 3A-3E; 64pp; English.  
 PS  
 XX A rat parathyroid hormone/parathyroid hormone-related protein  
 CC (PTH/PTHrP) receptor (AAR92277) is encoded by cDNA clone R15B  
 CC (AAT15947) isolated from a rat osteosarcoma ROS 17/2.8 cDNA library.  
 CC The receptor is a G-protein linked receptor having 7 transmembrane  
 CC domains. It induces an increase in intracellular cAMP and calcium  
 CC upon challenge with PTH or PTHrP. Recombinant receptor can be  
 CC produced in vector/host cell systems and used in the treatment,  
 CC diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia,  
 CC to screen for (ant)agonists and to raise antibodies. Host cells  
 CC expressing the receptor are used for diagnostic measurement of PTH  
 CC serum levels.  
 XX  
 SQ Sequence 591 AA;

Query Match 3.3%; Score 18; DB 17; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYH 262  
 |||||  
 Db 290 yflatnywilverglyh 307

RESULT 25  
 AAR73316  
 ID AAR73316 standard; Protein; 591 AA.  
 XX  
 AC AAR73316;  
 XX  
 XX 08-FEB-1999 (first entry)  
 XX  
 DE Parathyroid hormone receptor R15B.  
 XX  
 KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;  
 KW PTH-related hypercalcaemia; rat.  
 XX  
 OS Rattus sp.

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XX US5840853-A.
XX
XX PD 24-NOV-1998.
XX
XX PF 06-JUN-1995; 95US-0471494.
XX
XX PR 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX PR 06-JUN-1995; 95US-0471494.
XX
XX PA (GEHO ) GEN HOSPITAL CORP.
XX
XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
XX PI Schipani E, Segre GV;
XX
XX DR WPI; 1999-034124/03.
XX DR N-PSDB; AAV08390.
XX
XX PT Antibody to parathyroid hormone receptor - for diagnostic or
XX PT therapeutic use
XX
XX PS Claim 6; Fig 3; 63pp; English.
XX
XX CC This sequence represents the rat parathyroid hormone (PTH) receptor
XX CC R15B, which is targeted by the antibody of the invention. The antibody
XX CC of the invention is immunoreactive with naturally occurring human, rat or
XX CC opossum PTH receptor. The antibody is useful for treating disorders
XX CC characterised by overstimulation of PTH receptors by their ligand and for
XX CC the diagnosis of PTH-related hypercalcaemia.
XX
XX SQ Sequence 591 AA;

Query Match 3.3%; Score 18; DB 20; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
   |||||||
Db 290 yflatnywilvegylh 307

RESULT 26
AAR92278
ID AAR92278 standard; Protein; 593 AA.
XX
XX AC AAR92278;
XX
XX DT 18-MAY-1996 (first entry)
XX
XX DE Human kidney PTH/PTHrP receptor.
XX
XX KW Parathyroid hormone; receptor; parathormone; PTH;
XX KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
XX KW hypercalcaemia; hypocalcaemia; cancer.
XX
XX OS Homo sapiens.
XX
XX PN US5494806-A.
XX
XX PD 27-FEB-1996.
XX
XX PF 05-APR-1991; 91US-0681702.
XX
XX PR 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX
XX PA (GEHO ) GEN HOSPITAL CORP.
XX
XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
XX PI Schipani E, Segre GV;
XX

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DR WPI; 1996-139028/14.
DR N-PSDB; AAT15948.
XX
XX PT DNA encoding vertebrate parathyroid hormone receptor - useful for
XX PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
XX PT cancer etc.
XX
XX PS Claim 1; Fig 6A-6G; 64pp; English.
XX
XX CC A human parathyroid hormone/parathyroid hormone-related protein
XX CC (PTH/PTHrP) receptor (AAR92278) is encoded by cDNA clone HK-1
XX CC (AAT15948) isolated from a human kidney cDNA library. The receptor
XX CC induces an increase in intracellular cAMP and intracellular free
XX CC calcium when challenged by PTH or PTHrP. Recombinant receptor can
XX CC be produced in vector/host cell systems and used in the treatment,
XX CC diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia, to
XX CC screen for (ant)agonists and to raise antibodies. Host cells
XX CC expressing the receptor can be used for diagnostic measurement of
XX CC PTH serum levels.
XX
XX SQ Sequence 593 AA;

Query Match 3.3%; Score 18; DB 17; Length 593;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
   |||||||
Db 290 yflatnywilvegylh 307

RESULT 27
AAW73317
ID AAW73317 standard; Protein; 593 AA.
XX
XX AC AAW73317;
XX
XX DT 08-FEB-1999 (first entry)
XX
XX DE Human Parathyroid hormone receptor.
XX
XX KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
XX KW PTH-related hypercalcaemia; human.
XX
XX OS Homo sapiens.
XX
XX PN US5840853-A.
XX
XX PD 24-NOV-1998.
XX
XX PF 06-JUN-1995; 95US-0471494.
XX
XX PR 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX PR 06-JUN-1995; 95US-0471494.
XX
XX PA (GEHO ) GEN HOSPITAL CORP.
XX
XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
XX PI Schipani E, Segre GV;
XX
XX DR WPI; 1999-034124/03.
XX DR N-PSDB; AAV08391.
XX
XX PT Antibody to parathyroid hormone receptor - for diagnostic or
XX PT therapeutic use
XX
XX PS Claim 7; Fig 6; 63pp; English.
XX
XX CC This sequence represents the human parathyroid hormone (PTH) receptor
XX CC which is targeted by the antibody of the invention. The antibody
XX CC of the invention is immunoreactive with naturally occurring human, rat or

```

CC opossum PTH receptor. The antibody is useful for treating disorders  
CC characterised by overstimulation of PTH receptors by their ligand and for  
CC the diagnosis of PTH-related hypercalcaemia.

XX SQ Sequence 593 AA;

Query Match 3.3%; Score 18; DB 20; Length 593;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYH 262  
Db 290 yflatnywilverglyh 307

RESULT 28

AAB71876  
ID AAB71876 standard; Protein; 593 AA.

XX AC AAB71876;

XX DT 03-MAY-2001 (first entry)

XX DE Human PTHR seven transmembrane domain.

XX KW Human; parathyroid hormone/parathyroid hormone-related peptide receptor;  
KW PTHR; h15571; immunomodulatory; vascular; hepatic; antiasthma;  
KW antimicrobial; antinflammatory; immunosuppressive; gene therapy;  
KW vaccine; G-protein coupled receptor; GPCR; liver fibrosis;  
KW respiratory disorder; infection; chronic inflammatory disease;  
KW organ-specific autoimmunity; graft rejection; cystic fibrosis.

XX OS Homo sapiens.

XX PN WO200109328-A1.

XX PD 08-FEB-2001.

XX PF 03-AUG-2000; 2000WO-US21278.

XX PR 03-AUG-1999; 99US-0146916.

XX PR 29-FEB-2000; 2000US-0515781.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Hodge MR, Lloyd C, Welch NS;

XX PS WPI; 2001-138653/14.

XX CC Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful  
XX for preventing, diagnosing and treating, e.g. liver fibrosis and asthma

XX PS Disclosure; Fig 2; 145pp; English.

XX CC The present sequence is a human G-protein coupled receptor (GPCR) used  
XX for comparison with the seven transmembrane domain of a novel GPCR  
XX designated h15571. h15571 GPCR polynucleotides and polypeptides may be  
XX used in the prevention, treatment and diagnosis of diseases associated  
XX with inappropriate GPCR expression. Such diseases include immune,  
XX haematological, fibrotic, hepatic and respiratory disorders including  
XX asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic  
XX infections, chronic inflammatory diseases, organ-specific autoimmunity,  
XX graft rejection, graft versus host disease, cystic fibrosis and, in  
XX particular, liver fibrosis. The GPCR polypeptides may be used as antigens  
XX in the production of antibodies against GPCR and in assays to identify  
XX modulators (agonists and antagonists) of GPCR expression and activity.  
XX The anti-GPCR antibodies and GPCR antagonists may also be used to down  
XX regulate GPCR expression and activity. The anti-GPCR antibodies may be  
XX used as diagnostic agents for detecting the presence of GPCR  
XX polypeptides in samples.

SQ Sequence 593 AA;

Query Match 3.3%; Score 18; DB 22; Length 593;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYH 262  
Db 290 yflatnywilverglyh 307

RESULT 29

AAR27707  
ID AAR27707 standard; Protein; 614 AA.

XX AC AAR27707;

XX DT 16-MAR-1993 (first entry)

XX DE Human kidney PTH/PTHrP receptor.

XX KW Parathyroid hormone; related protein; calcium; antagonist;  
XX antibodies; hypercalcaemia.

XX OS Homo sapiens.

XX PN WO9217602-A.

XX PD 15-OCT-1992.

XX PF 06-APR-1992; 92WO-US02821.

XX PR 05-APR-1991; 91US-0681702.

XX PR 06-APR-1992; 92US-0864475.

XX PA (GEHO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.

XX PI Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;  
XX Segre GV;

XX DR WPI; 1992-366271/44.

XX DR N-PSDB; AAQ29607.

XX PT New DNA encoding parathyroid hormone receptor, DNA and antibodies  
XX - for (differential) diagnosis of hypercalcaemia, and diagnosis  
XX and treatment of tumours

XX PS Claim 22; Fig 6; 91pp; English.

XX CC The protein sequence was deduced from the cDNA sequence obtd by  
XX screening a human kidney oligo dT-primed cDNA library in lambda  
XX gt10 and a genomic library of human placental DNA in EMBL3 with a  
XX probe comprising most of the coding sequence of rat bone parathyroid  
XX hormone/parathyroid hormone related protein (PTH/PTHrP) receptor  
XX protein. The clone encodes a protein which may be used in a  
XX therapeutic compsn. to inhibit activation of PTH or PTHrP and thus  
XX reduce the level of calcium in the blood. Cps. capable of competing  
XX with PTH or PTHrP for binding can be identified using the protein prod.  
XX and DNAs homologous to PTH DNA can be identified using fragments of the  
XX clone as probes. The sequence may be used for the prodn. of antibodies  
XX useful for the treatment, classification, prognosis and/or treatment of  
XX disorders related to the interaction between a cell receptor and a  
XX ligand such as in hypercalcaemia. See also R27704-16.

XX SQ Sequence 614 AA;

Query Match 3.3%; Score 18; DB 13; Length 614;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYH 262

Db 290 yflatnnywilvegylh 307  
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## RESULT 30

AAR27710  
ID AAR27710 standard; peptide; 19 AA.

XX AC AAR27710;

XX DT 16-MAR-1993 (first entry)

XX DE PTH/PTHrP receptor fragment.

XX KW Parathyroid hormone; related protein; calcium; antagonist;  
XX KW antibodies; hypercalcaemia; extracellular domain.  
XX OS Synthetic.

XX PN W09217602-A.

XX PD 15-OCT-1992.

XX PF 06-APR-1992; 92WO-US02821.

XX PR 05-APR-1991; 91US-0681702.

XX PR 06-APR-1992; 92US-0864475.

XX PA (GEO ) GEN HOSPITAL CORP OFFICE TECHNOLOGY.

XX PI Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;

XX PI Segre GV;

XX DR WPI; 1992-366271/44.

XX PT New DNA encoding parathyroid hormone receptor, DNA and antibodies  
PT - for (differential) diagnosis of hypercalcaemia, and diagnosis  
PT and treatment of tumours  
XX PS Claim 25; Page 5; 91pp; English.  
XX CC The peptide sequence shown represents an extracellular fragment of  
CC parathyroid hormone/parathyroid hormone related protein  
CC (PTH/PTHrP) receptor protein. The peptide is capable of binding  
CC PTH or PTHrP and acting as an antagonist of these cpds. The  
CC peptide may be used to inhibit activation of PTH or PTHrP and thus  
CC reduce the level of calcium in the blood. Cods. capable of competing  
CC with PTH or PTHrP for binding can be identified using the protein prod.  
CC and DNAs homologous to PTH DNA can be identified using fragments of the  
CC clone as probes. The sequence may be used for the prodn. of antibodies  
CC useful for the treatment, classification, prognosis and/or treatment of  
CC disorders related to the interaction between a cell receptor and a  
CC ligand such as in hypercalcaemia. See also AAR27704-16.

XX SQ Sequence 19 AA;

Query Match 2.6%; Score 14; DB 13; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.1e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYYWILVEG 258

Db 6 yflatnnywilveg 19

|||||

## RESULT 31

AAR92281

ID AAR92281 standard; Peptide; 19 AA.

XX AC AAR92281;

XX DT 18-MAY-1996 (first entry)

XX PTH/PTHrP extracellular region fragment RP-3.

XX KW Parathyroid hormone; receptor; parathormone; PTH;

XX KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;  
XX KW hypercalcaemia; hypocalcaemia; cancer.

XX OS Synthetic.

XX PN US5494806-A.

XX PD 27-FEB-1996.

XX PF 05-APR-1991; 91US-0681702.

XX PR 06-APR-1992; 92US-0864475.

XX PR 05-APR-1991; 91US-0681702.

XX PA (GEO ) GEN HOSPITAL CORP.

XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;

XX PI Schipani E, Segre GV;

XX DR WPI; 1996-139028/14.

XX PT DNA encoding vertebrate parathyroid hormone receptor - useful for  
PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,  
PT cancer etc.  
XX PS Claim 21; Column 3; 64pp; English.  
XX CC Parathyroid hormone (PTH) receptor fragments, including those  
CC (AAR92279-84) based on the PTH extracellular region and those  
CC (AAR92285-87) based on the intracellular domain, are produced by  
CC incorporating encoding DNA sequences into a vector, and  
CC culturing cells transformed by the vector. The peptides can be  
CC used to raise antibodies. The peptides and antibodies are useful  
CC in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and  
CC hypocalcaemia, and can also be used to screen for (ant)agonists  
CC of therapeutic appln.

XX SQ Sequence 19 AA;

Query Match 2.6%; Score 14; DB 17; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.1e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYYWILVEG 258

Db 6 yflatnnywilveg 19

|||||

## RESULT 32

AAW73320

ID AAW73320 standard; peptide; 19 AA.

XX AC AAW73320;

XX DT 08-FEB-1999 (first entry)

XX DE Parathyroid hormone receptor fragment RP-3.

XX KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;

XX KW PTH-related hypercalcaemia; opossum; rat; human.

XX OS Synthetic.

XX PN US5840853-A.

XX PD 24-NOV-1998.

XX PF 06-JUN-1995; 95US-0471494.



XX PR 06-APR-1992; 92US-0864475.  
 XX PR 05-APR-1991; 91US-0681702.  
 XX PR 06-JUN-1995; 95US-0471494.  
 XX (GEO) GEN HOSPITAL CORP.  
 XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;  
 PI Schipani E, Segre GV;  
 XX WPI; 1999-034124/03.  
 XX Antibody to parathyroid hormone receptor - for diagnostic or  
 PT therapeutic use  
 PT Claim 8; Column 19; 63pp; English.  
 XX This sequence is a fragment of a opossum parathyroid hormone (PTH)  
 CC receptor which is targeted by the antibody of the invention. The antibody  
 CC of the invention is immunoreactive with naturally occurring human, rat or  
 CC opossum PTH receptor. The antibody is useful for treating disorders  
 CC characterised by overstimulation of PTH receptors by their ligand and for  
 CC the diagnosis of PTH-related hypercalcaemia.  
 XX SQ Sequence 19 AA;  
 Query Match 2.68; Score 14; DB 20; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-07;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 245 YFLATNYWILVEG 258  
 Db 6 yflatnywilverg 19  
 RESULT 33  
 AAB71878  
 ID AAB71878 standard; Protein; 457 AA.  
 XX AC AAB71878;  
 XX 03-MAY-2001 (first entry)  
 XX Human VIPR seven transmembrane domain.  
 XX Human; h15571; immunomodulatory; vascular; hepatic; hepatic; antiasthma; VIPR;  
 KW pituitary adenylate cyclase activating polypeptide type II receptor;  
 KW antimicrobial; antiinflammatory; immunosuppressive; gene therapy;  
 KW vaccine; G-protein coupled receptor; GPCR; liver fibrosis;  
 KW respiratory disorder; infection; chronic inflammatory disease;  
 KW organ-specific autoimmunity; graft rejection; cystic fibrosis.  
 XX OS Homo sapiens.  
 XX WO200109328-A1.  
 XX 08-FEB-2001.  
 XX 03-AUG-2000; 2000WO-US21278.  
 XX 03-AUG-1999; 99US-0146916.  
 XX 29-FEB-2000; 2000US-0515781.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX Hodge MR, Lloyd C, Welch NS;  
 XX WPI; 2001-138653/14.  
 XX Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful  
 PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma

XX Disclosure; Fig 2; 145pp; English.  
 XX The present sequence is a human G-protein coupled receptor (GPCR) used  
 CC for comparison with the seven transmembrane domain of a novel GPCR  
 CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be  
 CC used in the prevention, treatment and diagnosis of diseases associated  
 CC with inappropriate GPCR expression. Such diseases includes immune,  
 CC haematological, fibrotic, hepatic and respiratory disorders including  
 CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic  
 CC infections, chronic inflammatory diseases, organ-specific autoimmunity,  
 CC graft rejection, graft versus host disease, cystic fibrosis and, in  
 CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens  
 CC in the production of antibodies against GPCR and in assays to identify  
 CC modulators (agonists and antagonists) of GPCR expression and activity.  
 CC The anti-GPCR antibodies and GPCR antagonists may also be used to down  
 CC regulate GPCR expression and activity. The anti-GPCR antibodies may be  
 CC used as diagnostic agents for detecting the presence of GPCR  
 CC polypeptides in samples.  
 XX SQ Sequence 457 AA;  
 Query Match 2.4%; Score 13; DB 22; Length 457;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 172 LHCTRNYYTHMLHF 184  
 Db 170 lhctrnyihmhlf 182  
 RESULT 34  
 AAR72506  
 ID AAR72506 standard; Protein; 458 AA.  
 XX AC AAR72506;  
 XX 29-NOV-1995 (first entry)  
 XX Porcine vasoactive intestinal peptide receptor protein.  
 XX Porcine vasoactive intestinal peptide receptor; pig; lung tissue; probe;  
 KW amplification; primer; PCR; vasodilation; gastrointestinal tract.  
 XX OS Sus scrofa.  
 XX EP648837-A.  
 XX 19-APR-1995.  
 XX 24-AUG-1994; 94EP-0306251.  
 XX 25-AUG-1993; 93US-0112817.  
 XX (ELIL) LILLY & CO ELI.  
 XX Hsiung HM, Smith DP, Zhang X;  
 XX WPI; 1995-148716/20.  
 XX N-PSDB; AAQ89546.  
 XX Porcine vasoactive intestinal peptide receptor and DNA - useful in  
 PT receptor bio:activity assay and to screen for agents which inhibit or  
 PT stimulate receptor activity  
 XX Claim 3; Page 24-26; 35pp; English.  
 XX The amino acid sequence of the novel porcine vasoactive intestinal  
 CC peptide (pVIP) receptor. The gene was isolated from a cDNA library  
 CC in the Superscript (RTM) Lambda System derived from porcine lung tissue  
 CC RNA using a 700 bp probe amplified from lung tissue cDNA using primers  
 CC AAQ89547-8. The gene was inserted into the plasmid pSPORT for

CC sequencing. Thereafter the gene was inserted into the plasmid pRC/CMV  
 CC for transfection of 293 cells and production of the recombinant protein.  
 CC The activity of pVIP is linked to vasodilation in the lungs and  
 CC gastrointestinal tract. The receptor is useful in a bioactivity assay  
 CC for quantifying the level of stimulation and repression of pVIP  
 CC enzymatic activity in response to test compounds. The receptor is also  
 CC useful in screening for pVIP receptor inhibitory or stimulatory agents.  
 XX  
 SQ Sequence 458 AA;

Query Match 2.4%; Score 13; DB 16; Length 458;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNHYHMLF 184  
 Db 171 lhctnrnylhmlf 183

RESULT 35  
 AAR42848  
 ID AAR42848 standard; Protein; 459 AA.  
 AC AAR42848;

DT 13-MAY-1994 (first entry)  
 DE VIP receptor protein.  
 XX  
 XX vasoactive intestinal polypeptide receptor; VIP; rat; binding;  
 KW adenylate cyclase activity; stimulus.  
 XX

OS Rattus rattus.  
 XX  
 XX JP05255394-A.  
 PN  
 XX  
 PD 05-OCT-1993.  
 PF  
 PF 13-FEB-1992; 92JP-0026607.  
 PR 13-FEB-1992; 92JP-0026607.  
 XX  
 PA (OSAB-) 2H OSAKA BIOSCIENCE KENKYUSHO.  
 XX  
 XX WPI; 1993-348480/44.  
 DR N-PSDB; AAQ50349.  
 XX

PT Vasoactive intestinal polypeptide - prepd. in large amt. by  
 PT culturing microbe transformed by new DNA coding polypeptide  
 PS Claim 2; Page 6; 14pp; Japanese.  
 XX  
 XX The sequence can be used to produce large amounts of the VIP  
 CC receptor peptide, by culturing a microorganism transformed by  
 CC the sequence.  
 XX

SQ Sequence 459 AA;

Query Match 2.4%; Score 13; DB 14; Length 459;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNHYHMLF 184  
 Db 171 lhctnrnylhmlf 183

RESULT 36  
 AAY82704  
 ID AAY82704 standard; protein; 445 AA.  
 XX

AC AAY82704;  
 DT 11-AUG-2000 (first entry)  
 XX  
 DE Human glucose-dependent insulinotropic peptide receptor protein sequence.  
 XX  
 XX Human; glucose-dependent insulinotropic peptide receptor; GIPR;  
 KW GIP receptor; osteotropic hormone; bone; osteoblast; osteoporosis;  
 KW bone density; bone formation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200020592-A1.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 07-OCT-1999; 99WO-US23365.  
 XX  
 PR 07-OCT-1998; 98US-0103333.  
 PR 08-OCT-1998; 98US-0103495.  
 XX  
 PA (MEDI-) MEDICAL COLLEGE GEORGIA RES INST.  
 XX  
 PI Isales CM, Bollag RJ, Rasmussen H;  
 XX  
 DR WPI; 2000-303777/26.  
 XX  
 XX Maintaining or increasing bone density or formation for patients at  
 PT risk of osteoporosis comprises administering glucose-dependent  
 PT insulinotropic peptide -  
 XX  
 PS Example 2; Fig 6; 50pp; English.  
 XX  
 XX The present invention describes a method for maintaining or increasing  
 CC bone density or formation comprising administering to an individual a  
 CC glucose-dependent insulinotropic peptide (GIP) or a functionally  
 CC equivalent analogue. Also described are: (1) a transgenic non-human  
 CC mammal overexpressing GIP; and (2) a method for decreasing bone density  
 CC comprising administering to an individual an inhibitor of GIP binding to  
 CC the GIP receptor. The method is useful for maintaining or increasing  
 CC bone density and promoting bone formation in patients at risk of  
 CC osteoporosis. The present sequence represents the human GIP receptor  
 CC protein sequence, which is used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 445 AA;

Query Match 2.2%; Score 12; DB 21; Length 445;  
 Best Local Similarity 100.0%; Pred. No. 0.0012;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNHYH 180  
 Db 141 frllhctnrnylh 152

RESULT 37  
 AAY51528  
 ID AAY51528 standard; protein; 458 AA.  
 XX  
 AC AAY51528;  
 XX  
 DT 15-MAY-2000 (first entry)  
 XX  
 DE Human GIP receptor protein variant.  
 XX  
 KW GIP receptor; glucose-dependent insulinotropic polypeptide; human;  
 KW pancreatic beta cell; diabetes mellitus; transgenic animal.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP979872-A1.

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XX PD 16-FEB-2000.
XX PF 11-AUG-1999; 99EP-0115140.
XX PR 11-AUG-1998; 98DE-1036382.
XX PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX PA (WOLF/) WOLF E.
XX PI Peters H, Balling R, Volz A, Goetze B, Wolf E;
XX DR WPI; 2000-162923/15.
XX PT Recombinant GIP (Glucose dependent insulinotropic polypeptide) receptor
XX PT protein used as a model for investigation of development and treatment
XX PT of diabetes mellitus -
XX PS Claim 4; Page 11-12; 24pp; German.
XX CC This invention describes a novel recombinant GIP (Glucose-dependent
XX CC insulinotropic/insulin releasing polypeptide) receptor protein (I) or
XX CC an active fragment of (I), which binds to the GIP peptide hormone without
XX CC initiating a signal transduction cascade. The invention also describes a
XX CC (1) a recombinant DNA molecule (II), encoding (I) or its active fragment,
XX CC comprising: (a) a promoter that is in the beta cells of the pancreas;
XX CC (b) a sequence that is capable of binding to the GIP peptide hormone
XX CC without initiating a signal transduction cascade; (c) a termination
XX CC sequence; and (d) a polyadenylated tail sequence, where the expression of
XX CC (II) in a suitable host causes a diabetes type phenotype. (2) a vector
XX CC containing (II) or (III); (3) a eukaryotic or prokaryotic cell line (IV),
XX CC containing (II) or (III); (4) a transgenic, non human animal (V),
XX CC containing (II); and (5) preparing (V). (V) is used as a model system for
XX CC the investigation of the development, treatment and consequences of
XX CC diabetes mellitus. Several animal models for the study of diabetes have
XX CC been developed, but the use of (I) in a transgenic animal demonstrates of
XX CC the role of a defective GIP receptor in the development of diabetes,
XX CC which has not been shown before. This sequence represents the human GIP
XX CC receptor protein variant which has a deleted intracellular loop
XX CC region described in the method of the invention.
XX SQ Sequence 458 AA;

Query Match 2.2%; Score 12; DB 21; Length 458;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRRHLCTRNYIH 180
Db 162 frhlctrnyih 173

RESULT 38
AAY51526
ID AAY51526 standard; protein; 466 AA.
XX AC AAY51526;
XX DT 15-MAY-2000 (first entry)
XX DE Human GIP receptor protein.
XX KW GIP receptor; glucose-dependent insulinotropic polypeptide; human;
XX KW pancreatic beta cell; diabetes mellitus; transgenic animal.
XX OS Homo sapiens.
XX PN EP979872-A1.
XX PD 16-FEB-2000.
XX PF 11-AUG-1999; 99EP-0115140.

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XX 11-AUG-1998; 98DE-1036382.
XX PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX PA (WOLF/) WOLF E.
XX PI Peters H, Balling R, Volz A, Goetze B, Wolf E;
XX DR WPI; 2000-162923/15.
XX PT Recombinant GIP (Glucose dependent insulinotropic polypeptide) receptor
XX PT protein used as a model for investigation of development and treatment
XX PT of diabetes mellitus -
XX PS Disclosure; Page 9-10; 24pp; German.
XX CC This invention describes a novel recombinant GIP (Glucose-dependent
XX CC insulinotropic/insulin releasing polypeptide) receptor protein (I) or
XX CC an active fragment of (I), which binds to the GIP peptide hormone without
XX CC initiating a signal transduction cascade. The invention also describes a
XX CC (1) a recombinant DNA molecule (II), encoding (I) or its active fragment,
XX CC comprising: (a) a promoter that is in the beta cells of the pancreas;
XX CC (b) a sequence that is capable of binding to the GIP peptide hormone
XX CC without initiating a signal transduction cascade; (c) a termination
XX CC sequence; and (d) a polyadenylated tail sequence, where the expression of
XX CC (II) in a suitable host causes a diabetes type phenotype. (2) a vector
XX CC containing (II); (3) a eukaryotic or prokaryotic cell line (IV),
XX CC containing (II) or (III); (4) a transgenic, non human animal (V),
XX CC containing (II); and (5) preparing (V). (V) is used as a model system for
XX CC the investigation of the development, treatment and consequences of
XX CC diabetes mellitus. Several animal models for the study of diabetes have
XX CC been developed, but the use of (I) in a transgenic animal demonstrates of
XX CC the role of a defective GIP receptor in the development of diabetes,
XX CC which has not been shown before. This sequence represents the human GIP
XX CC receptor protein described in the method of the invention.
XX SQ Sequence 466 AA;

Query Match 2.2%; Score 12; DB 21; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRRHLCTRNYIH 180
Db 162 frhlctrnyih 173

RESULT 39
AAB71870
ID AAB71870 standard; Protein; 466 AA.
XX AC AAB71870;
XX DT 03-MAY-2001 (first entry)
XX DE Human GIPR seven transmembrane domain.
XX KW Human; GIPR; glucose-dependent insulinotropic polypeptide receptor;
XX KW h15571; immunomodulatory; vascular; hepatic; antiasthma; antimicrobial;
XX KW antiinflammatory; immunosuppressive; gene therapy; vaccine;
XX KW G-protein coupled receptor; GPCR; liver fibrosis;
XX KW respiratory disorder; infection; chronic inflammatory disease;
XX KW organ-specific autoimmunity; graft rejection; cystic fibrosis.
XX OS Homo sapiens.
XX PN WO200109328-A1.
XX PD 08-FEB-2001.
XX PF 03-AUG-2000; 2000WO-US21278.

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PR 03-AUG-1999; 99US-0146916.  
 PR 29-FEB-2000; 2000US-0515781.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX Hodge MR, Lloyd C, Welch NS;  
 PI WPI; 2001-138653/14.  
 XX Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful  
 XX for preventing, diagnosing and treating, e.g. liver fibrosis and asthma  
 PT -  
 PT  
 XX  
 PS Disclosure; Fig 2; 145pp; English.  
 XX The present sequence is a human G-protein coupled receptor (GPCR) used  
 CC for comparison with the seven transmembrane domain of a novel GPCR  
 CC designated h1571. h1571 GPCR polynucleotides and polypeptides may be  
 CC used in the prevention, treatment and diagnosis of diseases associated  
 CC with inappropriate GPCR expression. Such diseases includes immune,  
 CC haematological, fibrotic, hepatic and respiratory disorders including  
 CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic  
 CC infections, chronic inflammatory diseases, organ-specific autoimmunity,  
 CC graft rejection, graft versus host disease, cystic fibrosis and, in  
 CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens  
 CC in the production of antibodies against GPCR and in assays to identify  
 CC modulators (agonists and antagonists) of GPCR expression and activity.  
 CC The anti-GPCR antibodies and GPCR antagonists may also be used to down  
 CC regulate GPCR expression and activity. The anti-GPCR antibodies may be  
 CC used as diagnostic agents for detecting the presence of GPCR  
 CC polypeptides in samples.  
 XX  
 XX Sequence 466 AA;  
 SQ

Query Match 2.2%; Score 12; DB 22; Length 466;  
 Best Local Similarity 100.0%; Pred. No. 0.0012;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 169 FRLHCTRNVIH 180  
 DB 162 frrlhctrnvih 173  
 |||||

RESULT 40  
 AAR70138  
 ID AAR70138 standard; Peptide; 11 AA.  
 XX  
 AC AAR70138;  
 XX  
 DT 09-OCT-1995 (first entry)  
 XX  
 DE Opossum parathyroid hormone transmembrane domain.  
 XX  
 KW Secretin family; G-protein linked receptor; transmembrane domain.  
 XX  
 OS Opossum.  
 XX  
 PN W09506724-A.  
 XX  
 PD 09-MAR-1995.  
 XX  
 PF 01-SEP-1994; 94WO-GB01892.  
 XX  
 PR 01-SEP-1993; 93GB-0018105.  
 XX  
 PA (WEDI-) MEDICAL RES COUNCIL.  
 XX  
 PI Harmar AJ, Lutz EM, West KM;  
 XX  
 DR WPI; 1995-115440/15.  
 DR N-PSDB; AAQ83212.  
 XX

PT New nucleic acid encoding vasoactive intestinal peptide receptor  
 PT - and related polypeptides, vectors, transformed cells, probes  
 PT and antibodies, useful for diagnosis and for screening potential  
 XX agonists and antagonists.  
 PS Disclosure; Figure 3; 39pp; English.  
 XX  
 CC VIP2 is an adenylate cyclase-linked VIP receptor from rat brain. The  
 CC VIP2 receptor was identified by PCR of rat pituitary cDNA using  
 CC degenerate oligo primers corresp. to the third and seventh  
 CC transmembrane domains of the secretin family of G-protein linked  
 CC receptors (Q83212 and Q83213 respectively). The primers were based  
 CC on the third and seventh transmembrane domains of the rat secretin,  
 CC pig calcitonin and opossum parathyroid hormone (PTH) receptors (see  
 CC R70137-R701410. Full length cDNAs were isolated from an olfactory  
 CC bulb cDNA library. The sequence has been submitted to the EMBL/GenBank  
 CC database under accession No. 225885 (see Q83211/R70136). A  
 CC polynucleotide probe comprising a labelled DNA or RNA sequence  
 CC capable of specifically binding to a gene for VIP2 receptor is  
 CC claimed.  
 XX  
 XX Sequence 11 AA;  
 SQ

Query Match 2.0%; Score 11; DB 16; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00044;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 250 NYWVILVEGLY 260  
 DB 1 nywvilegly 11  
 |||||

RESULT 41  
 AAY90231  
 ID AAY90231 standard; Protein; 523 AA.  
 XX  
 AC AAY90231;  
 XX  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE Zebrafish PTH3R receptor protein sequence.  
 XX  
 KW Zebrafish; PTH1R receptor; PTH3R receptor; diagnosis; cancer;  
 KW parathyroid hormone type 1 receptor; parathyroid hormone type 3 receptor.  
 OS Brachydanio rerio.  
 XX  
 PN W0200032771-A1.  
 XX  
 PD 08-JUN-2000.  
 XX  
 PF 28-MAY-1999; 99WO-US11883.  
 XX  
 PR 30-NOV-1998; 98US-0110467.  
 XX  
 PA (JUEP/) JUEPPNER H.  
 PA (RUBI/) RUBIN D A.  
 XX  
 PI Jueppner H, Rubin DA;  
 XX  
 DR WPI; 2000-412319/35.  
 DR N-PSDB; AAA30829.  
 XX  
 PT Novel zebrafish parathyroid hormone/parathyroid hormone related peptide  
 PT receptor 3 and isolated nucleic acid encoding zebrafish parathyroid  
 PT hormone receptor 1 for treating disorders associated with receptor  
 PT function -  
 XX  
 PS Claim 38; Fig 2b; 111pp; English.  
 XX  
 CC This sequence is a parathyroid hormone receptor type 3 (PTH3R)  
 CC receptor protein of the invention. The invention also relates to a PTH1R

CC receptor protein. Antagonists of PTHrP or PTH3R can be used for the  
 CC treatment of diseases associated with an increase in PTHrP or PTH3R  
 CC activity, respectively. The peptides are used for diagnosis or prognosis  
 CC of diseases and disorders associated with PTH3R or PTHrP, such as cancer.  
 CC The polypeptides can be used as a molecular weight markers on sodium  
 CC dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) gels, or  
 CC on molecular sieve gel filtration columns. Antigenic epitope-bearing  
 CC peptides and polypeptides are useful to raise antibodies, including  
 CC monoclonal antibodies, that bind specifically to a polypeptide. The  
 CC peptides are useful during diagnosis of diseases and disorders in  
 CC mammals involving PTHrP or PTH3R receptor expression or function.  
 CC Mutations that affect PTHrP or PTH3R sequence and/or expression levels  
 CC of PTHrP or PTH3R could be diagnostic for patients with disease or  
 CC disorders of a developmental, physiological or neurological nature. The  
 CC nucleic acid molecules are valuable for chromosome identification. The  
 CC mapping of DNAs to chromosomes is an important first step in  
 CC correlating those sequences with genes associated with disease.  
 XX  
 SQ Sequence 523 AA;

Query Match 2.0%; Score 11; DB 21; Length 523;  
 Best Local Similarity 100.0%; Pred. No. 0.014; Mismatches 0; Indels 0; Gaps 0;  
 Matches 11; Conservative 0;

QY 252 YWILVEGLYLH 262  
 |||||  
 DB 236 ywilverglylh 246

## RESULT 42

AAY99601  
 ID AAY99601 standard; Protein; 542 AA.

AC AAY99601;

XX 27-OCT-2000 (first entry)

DE Zebrafish parathyroid hormone type-3 receptor PTH3R.

KW Zebrafish; parathyroid hormone type-3 receptor; PTH3R;  
 KW developmental disorder; physiological disorder; neurological disorder.

OS Brachydanio rerio.

PN WO200032775-A1.

XX 08-JUN-2000.

PF 30-NOV-1999; 99WO-US28207.

PR 30-NOV-1998; 98US-0110467.

PA (JUEP/) JUEPPNER H.

FA (RUBI/) RUBIN D A.

PI Jueppner H, Rubin DA;

DR WPI; 2000-412323/35.

XX N-PSDB; AAA48446.

PT New nucleic acids encoding parathyroid hormone receptors PTHrP and  
 PT PTH3R, useful for treating diseases or disorders associated with  
 PT impaired receptor functions comprises a specific nucleotide sequence -

PS Claim 23; Fig 2B; 11lpp; English.

XX The present sequence is the parathyroid hormone type-3 receptor  
 CC (PTH3R) from the zebrafish. Its coding sequence was obtained by  
 CC sequencing a cDNA clone. The gene and protein can be used to detect  
 CC diseases in man where the receptor is either overexpressed or  
 CC underexpressed, and they can be used to treat these diseases, which may  
 CC be developmental, physiological or neurological disorders. They can also

CC be used to identify agonists and antagonists which can be used in a  
 CC similar manner. In addition, the gene can be used for chromosome  
 CC identification.

SQ Sequence 542 AA;

Query Match 2.0%; Score 11; DB 21; Length 542;  
 Best Local Similarity 100.0%; Pred. No. 0.015;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 YWILVEGLYLH 262  
 |||||  
 DB 236 ywilverglylh 246

## RESULT 43

AAR92285  
 ID AAR92285 standard; Peptide; 10 AA.

XX AAR92285;

XX 18-MAY-1996 (first entry)

DE PTH/PTHrP intracellular region fragment RPI-7.

KW Parathyroid hormone; receptor; parathormone; PTH;  
 KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;  
 KW hypercalcaemia; hypocalcaemia; cancer.

OS Synthetic.

PN US5494806-A.

XX 27-FEB-1996.

PF 05-APR-1991; 91US-0681702.

PR 06-APR-1992; 92US-0864475.

XX 05-APR-1991; 91US-0681702.

PA (GEHO ) GEN HOSPITAL CORP.

XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;

PI Schipani E, Segre GV;

XX WPI; 1996-139028/14.

PT DNA encoding vertebrate parathyroid hormone receptor - useful for  
 PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,  
 PT cancer etc.

XX Disclosure; Column 3; 64pp; English.

XX Parathyroid hormone (PTH) receptor fragments, including those  
 CC (AAR92279-84) based on the PTH extracellular region and those  
 CC (AAR92285-87) based on the intracellular domain, are produced by  
 CC incorporating encoding DNA sequences into a vector, and  
 CC culturing cells transformed by the vector. The peptides can be  
 CC used to raise antibodies. The peptides and antibodies are useful  
 CC in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and  
 CC hypocalcaemia, and can also be used to screen for (ant)agonists  
 CC of therapeutic appln.

SQ Sequence 10 AA;

Query Match 1.8%; Score 10; DB 17; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0043;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRHLCTRYN 178  
 |||||

```

Db      1 frrlhcrrny 10

RESULT 44
AAR57829
ID AAR57829 standard; Protein; 162 AA.
XX
AC AAR57829;
XX
DT 03-OCT-1994 (first entry)
XX
DE Human GR C-terminal (clone 40-2-2).
XX
KW Rat; human; glucagon receptor; transgenic animal; metabolism; model;
KW amplification; primer; polymerase chain reaction; PCR.
XX
OS Homo sapiens.
XX
PN WO9405789-A.
XX
PD 17-MAR-1994.
XX
PF 30-AUG-1993; 93WO-US08174.
XX
PR 28-AUG-1992; 92US-0938331.
PR 01-JUL-1993; 93US-0086631.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Foster DC, Grant FJ, Jelinek LJ, Kindsvogle WR;
PI Kuijper JL, Lok S, O'Hara PJ, Sheppard PO;
XX
DR WPI: 1994-101194/12.
DR N-PSDB; AAQ67247.
XX
XX New recombinant glucagon receptors and antibodies - useful to
PT produce model transgenic animals for study and with therapeutic
PT applications
XX
PS Example 5; Page 86-87; 112pp; English.
XX
CC Example 5 describes the isolation of human GR.
CC The GR coding sequence was constructed from partial clone
CC p9A11 (5' end) and clone 40-2-2 (3' end).
CC Host cells contg. GR DNA may be used for the prodn. of
CC recombinant GR. GR DNA may also be expressed in non-human
CC transgenic animals, pref. mice. Such animals may be readily
CC used as models to study the role of the glucagon receptor
CC in metabolism.
XX
SQ Sequence 162 AA;

Query Match 1.8%; Score 10; DB 15; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
DB 99 lveglylhl 108
|||||

RESULT 45
AAW68067
ID AAW68067 standard; Protein; 222 AA.
XX
AC AAW68067;
XX
DT 23-SEP-1998 (first entry)
XX
DE Human glucagon-like peptide-2 (GLP-2) receptor fragment.
XX
KW Glucagon-like peptide-2 receptor; GLP-2 receptor; human; rat;

receptor ligand screening.
KW
XX Homo sapiens.
XX
PN WO9825955-A2.
XX
PD 18-JUN-1998.
XX
PF 15-DEC-1997; 97WO-CA00969.
XX
PR 24-APR-1997; 97US-0845546.
PR 13-DEC-1996; 96US-0767224.
PR 24-JAN-1997; 97US-0787721.
XX
PA (ALIX ) ALLELIX BIOPHARMACEUTICALS INC.
XX
PI Fan E, Gupta AK, McCallum K, Munroe DG, Vyas TB;
XX
DR WPI: 1998-348449/30.
DR N-PSDB; AAV39157.
XX
PT New, e.g. rat glucagon-like peptide-2 receptor - useful for, e.g.
PT isolating homologues and GLP-2 receptor ligand screening
XX
PS Disclosure; Fig 5; 54pp; English.
XX
CC This is a human glucagon-like peptide-2 (GLP-2) receptor fragment. The
CC specification provides the sequences of human and rat GLP-2 receptors.
CC Genetically engineered host cells containing the GLP-2 receptor encoding
CC nucleic acid sequences operably linked to expression elements can be
CC used to produce the recombinant proteins. These cells can be used in a
CC method for identifying GLP-2 receptor ligands which comprises incubating
CC a candidate ligand with the cell, and determining whether binding has
CC occurred between the GLP-2 receptor and the candidate ligand. The GLP-2
CC receptor polynucleotides can be used to isolate GLP-2 receptor-encoding
CC homologues. They can also be used for constructing cell lines for GLP-2
CC receptor ligand screening.
XX
SQ Sequence 222 AA;

Query Match 1.8%; Score 10; DB 19; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHM 181
DB 20 lhctrnylhm 29
|||||

RESULT 46
AAR50047
ID AAR50047 standard; Protein; 477 AA.
XX
AC AAR50047;
XX
DT 03-OCT-1994 (first entry)
XX
DE Human glucagon receptor.
XX
KW Rat; human; glucagon receptor; transgenic animal; metabolism; model;
KW signal sequence; transmembrane domain; glycosylation site.
XX
OS Homo sapiens.
XX
PN WO9405789-A.
XX
PD 17-MAR-1994.
XX
PF 30-AUG-1993; 93WO-US08174.
XX
PR 28-AUG-1992; 92US-0938331.
PR 01-JUL-1993; 93US-0086631.

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XX PA (ZYMO) ZYMOGENETICS INC.  
 XX PI Foster DC, Grant RJ, Jelinek LJ, Kindsvogle WR;  
 XX PI Kuijper JL, Lok S, O'Hara PJ, Sheppard PO;  
 XX DR WPI; 1994-101194/12.  
 XX DR N-PSDB; AAQ58776.  
 XX PT New recombinant glucagon receptors and antibodies - useful to  
 PT produce model transgenic animals for study and with therapeutic  
 PT applications  
 XX PS Claim 4; Page 91-95; 112pp; English.  
 XX CC Rat and human glucagon receptor (GR) DNA was isolated.  
 CC CC Host cells contg. GR DNA may be used for the prodn. of  
 CC CC recombinant GR. GR DNA may also be expressed in non-human  
 CC CC transgenic animals, pref. mice. Such animals may be readily  
 CC CC used as models to study the role of the glucagon receptor  
 CC CC in metabolism.  
 XX SQ Sequence 477 AA;

Query Match 1.8%; Score 10; DB 15; Length 477;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 LVEGLYLHNL 264  
 Db 243 lveglylhnl 252  
 |||||||||

## RESULT 47

AAB71872  
 ID AAB71872 standard; Protein; 477 AA.

XX AC AAB71872;

XX DT 03-MAY-2001 (first entry)

XX DE Human GLR seven transmembrane domain.

XX KW Human; GLR; glucagon receptor; h15571; immunomodulatory; vascular;  
 KW KW hepatic; antilasthma; antimicrobial; antiinflammatory; immunosuppressive;  
 KW KW gene therapy; vaccine; G-protein coupled receptor; GPCR; liver fibrosis;  
 KW KW respiratory disorder; infection; chronic inflammatory disease;  
 KW KW organ-specific autoimmunity; graft rejection; cystic fibrosis.

XX OS Homo sapiens.

XX PN W0200109328-A1.

XX PD 08-FEB-2001.

XX PF 03-AUG-2000; 2000WO-US21278.

XX PR 03-AUG-1999; 99US-0146916.

XX PR 29-FEB-2000; 2000US-0515781.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Hodge MR, Lloyd C, Weich NS;

XX DR WPI; 2001-138653/14.

XX PT Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful  
 PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma

XX PS Disclosure; Fig 2; 145pp; English.

CC The present sequence is a human G-protein coupled receptor (GPCR) used  
 CC for comparison with the seven transmembrane domain of a novel GPCR  
 CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be  
 CC used in the prevention, treatment and diagnosis of diseases associated  
 CC with inappropriate GPCR expression. Such diseases includes immune,  
 CC haematological, fibrotic, hepatic and respiratory disorders including  
 CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic  
 CC infections, chronic inflammatory diseases, organ-specific autoimmunity,  
 CC graft rejection, graft versus host disease, cystic fibrosis and, in  
 CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens  
 CC in the production of antibodies against GPCR and in assays to identify  
 CC modulators (agonists and antagonists) of GPCR expression and activity.  
 CC The anti-GPCR antibodies and GPCR antagonists may also be used to down  
 CC regulate GPCR expression and activity. The anti-GPCR antibodies may be  
 CC used as diagnostic agents for detecting the presence of GPCR  
 CC polypeptides in samples.

XX SQ Sequence 477 AA;

Query Match 1.8%; Score 10; DB 22; Length 477;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 LVEGLYLHNL 264  
 Db 243 lveglylhnl 252  
 |||||||||

## RESULT 48

AAW68066  
 ID AAW68066 standard; Protein; 550 AA.

XX AC AAW68066;

XX DT 23-SEP-1998 (first entry)

XX DE Rat glucagon-like peptide-2 (GLP-2) receptor.

XX KW Glucagon-like peptide-2 receptor; GLP-2 receptor; human; rat;  
 KW KW receptor ligand screening.

XX OS Rattus sp.

XX FH Key Location/Qualifiers  
 FT Peptide 1..66  
 FT Protein /note= "signal sequence"  
 FT /note= "mature protein"  
 FT 67..550

XX PN W09825955-A2.

XX PD 18-JUN-1998.

XX PF 15-DEC-1997; 97WO-CA00969.

XX PR 24-APR-1997; 97US-0845546.

XX PR 13-DEC-1996; 96US-0767224.

XX PR 24-JAN-1997; 97US-0787721.

XX PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.

XX PI Fan E, Gupta AK, McCallum K, Munroe DG, Vyas TB;

XX DR WPI; 1998-348449/30.

XX DR N-PSDB; AAV39156.

XX PT New, e.g. rat glucagon-like peptide-2 receptor - useful for, e.g.

XX PT isolating homologues and GLP-2 receptor ligand screening

XX PS Claim 16; Fig 2; 54pp; English.

XX This represents a rat glucagon-like peptide-2 (GLP-2) receptor. The

CC specification provides the sequences of human and rat GLP-2 receptors.  
CC Genetically engineered host cells containing the GLP-2 receptor encoding  
CC nucleic acid sequences operably linked to expression elements can be  
CC used to produce the recombinant proteins. These cells can be used in a  
CC method for identifying GLP-2 receptor ligands which comprises incubating  
CC a candidate ligand with the cell, and determining whether binding has  
CC occurred between the GLP-2 receptor and the candidate ligand. The GLP-2  
CC receptor polynucleotides can be used to isolate GLP-2 receptor-encoding  
CC homologues. They can also be used for constructing cell lines for GLP-2  
CC receptor ligand screening.  
XX  
SQ Sequence 550 AA;

Query Match 1.8%; Score 10; DB 19; Length 550;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHM 181  
| | | | | | | | | |  
Db 206 lhctrnyihm 215

RESULT 49  
AAW68065  
ID AAW68065 standard; Protein: 553 AA.  
XX  
AC AAW68065;  
XX  
DT 23-SEP-1998 (first entry)  
XX  
DE Human glucagon-like peptide-2 (GLP-2) receptor.  
XX  
KW Glucagon-like peptide-2 receptor; GLP-2 receptor; human; rat;  
KW receptor ligand screening.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..66  
FT /note= "signal sequence"  
FT Protein 67..553  
FT /note= "mature protein"  
XX  
PN WO9825955-A2.  
XX  
PD 18-JUN-1998.  
XX  
PF 15-DEC-1997; 97WO-CA00969.  
XX  
PR 24-APR-1997; 97US-0845546.  
PR 13-DEC-1996; 96US-0767224.  
PR 24-JAN-1997; 97US-0787721.  
XX  
PA (ALLX ) ALLELIX BIOPHARMACEUTICALS INC.  
XX  
PI Fan E, Gupta AK, McCallum K, Munroe DG, Vyas TB;  
XX  
DR WPI; 1998-348449/30.  
DR N-PSDB; AAV39155.  
XX  
PT New, e.g. rat glucagon-like peptide-2 receptor - useful for, e.g.  
PT Isolating homologues and GLP-2 receptor ligand screening  
XX  
PS Claim 17; Fig 6A-B; 54pp; English.  
XX

CC This represents a human glucagon-like peptide-2 (GLP-2) receptor. The  
CC specification provides the sequences of human and rat GLP-2 receptors.  
CC Genetically engineered host cells containing the GLP-2 receptor encoding  
CC nucleic acid sequences operably linked to expression elements can be  
CC used to produce the recombinant proteins. These cells can be used in a  
CC method for identifying GLP-2 receptor ligands which comprises incubating  
CC a candidate ligand with the cell, and determining whether binding has

CC occurred between the GLP-2 receptor and the candidate ligand. The GLP-2  
CC receptor polynucleotides can be used to isolate GLP-2 receptor-encoding  
CC homologues. They can also be used for constructing cell lines for GLP-2  
CC receptor ligand screening.  
XX  
SQ Sequence 553 AA;

Query Match 1.8%; Score 10; DB 19; Length 553;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHM 181  
| | | | | | | | | |  
Db 206 lhctrnyihm 215

Search completed: September 21, 2001, 17:09:55  
Job time: 203 sec







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 21, 2001, 17:08:32 ; Search time 19.6 Seconds  
(without alignments)  
2102.573 Million cell updates/sec

Title: US-09-236-468a-2  
Perfect score: 541  
Sequence: 1 MAWLGAHLVWGLMLGSL.....DDILAEKSPRMESNPDTBG 541

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues  
Word size: 10

Total number of hits satisfying chosen parameters: 17

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : PIR\_68: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	363	67.1	550	2 A57519	parathyroid hormon
2	25	4.6	585	2 A39286	parathyroid hormon
3	19	3.5	440	2 JC2532	secretin receptor
4	19	3.5	449	2 SI6319	secretin receptor
5	18	3.3	589	2 I59297	parathyroid' hormon
6	18	3.3	591	2 S44203	parathyroid' hormon
7	18	3.3	591	2 I54195	parathyroid' hormon
8	18	3.3	593	2 A49191	parathyroid' hormon
9	13	2.4	455	2 I53273	gastric inhibitory
10	13	2.4	459	2 JH0594	vasoactive intesti
11	13	2.4	460	2 JC2194	vasoactive intesti
12	13	2.4	462	2 JC2462	gastric inhibitory
13	13	2.4	495	2 JC2195	vasoactive intesti
14	12	2.2	466	2 G02234	gastric inhibitory
15	12	2.2	466	2 S66676	glucose-dependent
16	12	2.2	491	2 I37411	glucose-dependent
17	10	1.8	477	2 JC2041	glucagon receptor

ALIGNMENTS

RESULT 1  
A57519  
parathyroid hormone receptor 2 precursor - human  
N: Alternate names: PTH2 receptor  
C: Species: Homo sapiens (man)  
C: Date: 08-Dec-1995 #sequence\_revision 08-Dec-1995 #text\_change 24-Nov-1999  
C: Accession: A57519

R: Usdin, T.B.; Gruber, C.; Bonner, T.J.  
J. Biol. Chem. 270, 15455-15458, 1995.  
A: Title: Identification and functional expression of a receptor selectively recognizing  
A: Reference number: A57519; MUID: 95318121  
A: Accession: A57519  
A: Status: preliminary; nucleic acid sequence not shown  
A: Molecule type: mRNA  
A: Residues: 1-550 <USD>  
A: Cross-references: GB: U25128; NID: g887966; PIDN: AAC50157.1; PID: g887967  
C: Genetics:  
A: Gene: GDB: PTHR2; PTHR2R  
A: Cross-references: GDB: 731977; OMIM: 601469  
A: Map position: 2q33-2q33  
C: Superfamily: glucagon receptor  
C: Keywords: hormone receptor

Query Match 67.1%; Score 363; DB 2; Length 550;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 LGASLHVWGLMLGSCLLARAQLDSGTITIEEQIVLVKAKVQCELNITAQLOEGCNC 63  
Db 4 LGASLHVWGLMLGSCLLARAQLDSGTITIEEQIVLVKAKVQCELNITAQLOEGCNC 63  
Qy 64 FPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTNWYNS 123  
Db 64 FPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTNWYNS 123  
Qy 124 DCLRFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNVIHML 183  
Db 124 DCLRFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNVIHML 183  
Qy 184 FVSPMLRATSIYFVDRVVAHIGVKELESIMQDDPQNSIEATSDVKSOYIGCKTAVVWF 243  
Db 184 FVSPMLRATSIYFVDRVVAHIGVKELESIMQDDPQNSIEATSDVKSOYIGCKTAVVWF 243  
Qy 244 IYFLATNYWILVEGLYLHNLIFVAFSDTKYLMGFIIGWGFPAAFVAAVAVARATLAD 303  
Db 244 IYFLATNYWILVEGLYLHNLIFVAFSDTKYLMGFIIGWGFPAAFVAAVAVARATLAD 303  
Qy 304 ARCWELSGADIKWIYQAPILAAIGLNFILFNTVVRVLTATKIWETNAVGHDRKQYRKLAK 363  
Db 304 ARCWELSGADIKWIYQAPILAAIGLNFILFNTVVRVLTATKIWETNAVGHDRKQYRKLAK 363  
Qy 364 STLVLVLFVGVHYIVFVCLPHSFTGLGWEIRHCELFNSFGPFVSIYCYCNGEVOAE 423  
Db 364 STLVLVLFVGVHYIVFVCLPHSFTGLGWEIRHCELFNSFGPFVSIYCYCNGEVOAE 423  
Qy 424 VKMWSRNLSVDNKRTPPCGSRRCGSLVTVTHTSTSSQSOVAA 467  
Db 424 VKMWSRNLSVDNKRTPPCGSRRCGSLVTVTHTSTSSQSOVAA 467

RESULT 2  
A39286  
parathyroid hormone / parathyroid hormone-related peptide - North American opossum  
C: Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opo  
C: Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 11-Jan-2000  
C: Accession: A39286  
R: Jueppner, H.; Abou-Samra, A.B.; Freeman, M.; Kong, X.F.; Schipani, E.; Richards, J.  
Science 254, 1024-1026, 1991  
A: Title: A G protein-linked receptor for parathyroid hormone and parathyroid hormone-  
A: Reference number: A39286; MUID: 92054592  
A: Accession: A39286  
A: Status: preliminary; not compared with conceptual translation  
A: Molecule type: mRNA  
A: Residues: 1-585 <JUE>  
A: Cross-references: GB: M74445  
C: Superfamily: glucagon receptor  
C: Keywords: G protein-coupled receptor; transmembrane protein

—

A:Reference number: A42698; MUID:92212903  
A:Accession: A42698  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-585, 'G', 587-591 <ABO>  
A:Experimental source: ROS 17/2.8 osteosarcoma cells  
A:Note: sequence extracted from NCBI backbone (NCBIP:92187)  
C:Superfamily: glucagon receptor

Query Match 3.3%; Score 18; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 7.3e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262  
|||||  
Db 290 YFLATNYWILVEGLYLH 307

## RESULT 8

A49191  
N:parathyroid hormone/PTH-related peptide receptor - human  
N:Alternate names: parathyroid hormone/parathyroid hormone related peptide receptor  
C:Species: Homo sapiens (man)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 11-Jan-2000  
C:Accession: I38139; A49191; I38113; G01562; S29610  
R:Schipani, E.; Weinstein, L.S.; Bergwitz, C.; Iida-Klein, A.; Kong, X.F.; Stuhmann, M.  
Kronenberg, H.M.; Abou-Samra, A.B.; Segre, G.V.; Jueppner, H.  
J. Clin. Endocrinol. Metab. 80, 1611-1621, 1995  
A:Title: Pseudohypoparathyroidism type 1b is not caused by mutations in the coding exons  
A:Reference number: I38139; MUID:95263723  
A:Accession: I38139  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-593 <RES>  
A:Cross-references: EMBL:U22409; NID:g897594; PIDN:AAB60657.1; PID:g897596  
R:Schipani, E.; Karga, H.; Karapilis, A.C.; Potts Jr., J.T.; Kronenberg, H.M.; Segre, G.V.  
Endocrinology 132, 2157-2165, 1993  
A:Title: Identical complementary deoxyribonucleic acids encode a human renal and bone pa  
A:Reference number: A49191; MUID:93238641  
A:Accession: A49191  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-593 <SCH>  
A:Cross-references: GB:I04308; NID:g190721; PIDN:AAA36525.1; PID:g190722  
A:Note: sequence extracted from NCBI backbone (NCBIN:I30233, NCBIP:I30234)  
R:Schneider, H.; Feyen, J.H.; Seuwen, K.; Movva, N.R.  
Eur. J. Pharmacol. 246, 149-155, 1993  
A:Title: Cloning and functional expression of a human parathyroid hormone receptor.  
A:Reference number: I38113; MUID:93387403  
A:Accession: I38113  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-593 <REV>  
A:Cross-references: EMBL:X68596; NID:g396812; PIDN:CAA48589.1; PID:g396813  
R:Levine, M.  
submitted to the EMBL Data Library, November 1994  
A:Reference number: G07787  
A:Accession: G01562  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-593 <LEV>  
A:Cross-references: EMBL:U17418; NID:g596129; PIDN:AAA56774.1; PID:g596130  
C:Genetics: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2; 45  
A:Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2; 45  
C:Superfamily: glucagon receptor  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.3%; Score 18; DB 2; Length 593;  
Best Local Similarity 100.0%; Pred. No. 7.3e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262  
|||||  
Db 290 YFLATNYWILVEGLYLH 307

## RESULT 9

I53273  
gastric inhibitory polypeptide receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 24-Sep-1999  
C:Accession: I53273  
R:Uddin, T.B.; Mezey, E.; Button, D.C.; Brownstein, M.J.; Bonner, T.I.  
Endocrinology 133, 2861-2870, 1993  
A:Title: Gastric inhibitory polypeptide receptor, a member of the secretin-vasoactive  
A:Reference number: I53273; MUID:94062667  
A:Accession: I53273  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-455 <RES>  
A:Cross-references: GB:L19660; NID:g431448; PIDN:AAC37637.1; PID:g431449  
C:Superfamily: glucagon receptor

Query Match 2.4%; Score 13; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 7.6e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNTHM 181  
|||||  
Db 159 FRLHCTRNTHM 171

## RESULT 10

JH0594  
vasoactive intestinal peptide receptor precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
C:Accession: JH0594; S56014  
R:Ishihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.  
Neuron 8, 811-819, 1992  
A:Title: Functional expression and tissue distribution of a novel receptor for vasoac  
A:Reference number: JH0594; MUID:92232309  
A:Accession: JH0594  
A:Molecule type: mRNA  
A:Residues: 1-459 <ISH>  
A:Cross-references: GB:M86835; NID:g207640; PIDN:AAA42331.1; PID:g207641  
R:Pei, L.; Melmed, S.  
Biochem. J. 308, 719-723, 1995  
A:Title: Characterization of the rat vasoactive intestinal polypeptide receptor gene  
A:Reference number: S56014; MUID:97104266  
A:Accession: S56014  
A:Status: preliminary; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-26 <PEI>  
A:Cross-references: EMBL:U10635; NID:g505752; PIDN:AAB48185.1; PID:g514311  
C:Superfamily: glucagon receptor  
C:Keywords: G protein-coupled receptor; glycoprotein; intestine; transmembrane protel  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-459/Product: vasoactive intestinal polypeptide receptor #status predicted <SIG>  
F:146-168/Domain: transmembrane #status predicted <TM1>  
F:176-195/Domain: transmembrane #status predicted <TM2>  
F:218-241/Domain: transmembrane #status predicted <TM3>  
F:256-277/Domain: transmembrane #status predicted <TM4>  
F:295-318/Domain: transmembrane #status predicted <TM5>  
F:344-363/Domain: transmembrane #status predicted <TM6>  
F:376-395/Domain: transmembrane #status predicted <TM7>  
F:58,69,100,292/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.4%; Score 13; DB 2; Length 459;  
Best Local Similarity 100.0%; Pred. No. 7.6e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHMLF 184  
|||||  
Db 171 LHCTRNYIHMLF 183

RESULT 11  
JC2194  
vasoactive intestinal peptide receptor precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 28-Aug-1995 #sequence\_revision 07-Oct-1994 #text\_change 05-Nov-1999  
C:Accession: JC2194; JN0604; PC2289; S38397  
R:Couvineau, A.; Rouyer-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-Denis  
Biochem. Biophys. Res. Commun. 200, 769-776, 1994  
A:Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA en  
A:Reference number: JC2194; MUID:94235025  
A:Accession: JC2194  
A:Molecule type: mRNA  
A:Residues: 1-460 <COU>  
A:Cross-references: EMBL:X75299; NID:9407461; PIDN:CAA53046.1; PID:9407462  
A:Experimental source: jejunal epithelial cell; clone hIVR8  
R:Sreedharan, S.P.; Patel, D.R.; Huang, J.X.; Goetzl, E.J.  
Biochem. Biophys. Res. Commun. 193, 546-553, 1993  
A:Title: Cloning and functional expression of a human neuroendocrine vasoactive intestin  
A:Reference number: JN0604; MUID:93290641  
A:Accession: JN0604  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-284,288-460 <SRE>  
A:Cross-references: GB:L13288; NID:9292903; PIDN:AAA36805.1; PID:g292904  
R:Couvineau, A.; Gaudin, P.; Maoret, J.J.; Rouyer-Fessard, C.; Nicole, P.; Laburthe, M.  
Biochem. Biophys. Res. Commun. 206, 246-252, 1995  
A:Title: Highly conserved aspartate 68, tryptophane 73 and glycine 109 in the N-terminal  
A:Reference number: PC2289; MUID:95118345  
A:Accession: PC2289  
A:Molecule type: mRNA  
A:Residues: 63-129 <CO2>  
C:Genetics:  
A:Gene: GDB:VIPR1; RCD1; HVRI  
A:Cross-references: GDB:128589; OMIM:192321  
A:Map position: 3p22-3p22  
C:Superfamily: glucagon receptor  
C:Keywords: glycoprotein; hormone receptor; intestine; phosphoprotein; transmembrane pro  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-460/Product: vasoactive intestinal peptide receptor #status predicted <MAT>  
F:145-168/Domain: transmembrane #status predicted <TM1>  
F:176-194/Domain: transmembrane #status predicted <TM2>  
F:216-234/Domain: transmembrane #status predicted <TM3>  
F:253-277/Domain: transmembrane #status predicted <TM4>  
F:299-319/Domain: transmembrane #status predicted <TM5>  
F:346-363/Domain: transmembrane #status predicted <TM6>  
F:377-396/Domain: transmembrane #status predicted <TM7>  
F:58,69,100,293/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:76/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted  
F:250/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted  
F:450/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 2.4%; Score 13; DB 2; Length 460;  
Best Local Similarity 100.0%; Pred. No. 7.7e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHMLF 184  
|||||  
Db 170 LHCTRNYIHMLF 182

RESULT 12  
JC2462  
gastric inhibitory polypeptide receptor - hamster  
N:Alternate names: GIP receptor  
C:Species: Cricetinae gen. sp. (hamster)  
C:Date: 15-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 20-Jun-2000

C:Accession: JC2462  
R:Yasuda, K.; Inagaki, N.; Yamada, Y.; Kubota, A.; Seino, S.; Seino, Y.  
Biochem. Biophys. Res. Commun. 205, 1556-1562, 1994  
A:Title: Hamster gastric inhibitory polypeptide receptor expressed in pancreatic isle  
A:Reference number: JC2462; MUID:95110292  
A:Accession: JC2462  
A:Molecule type: mRNA  
A:Residues: 1-462 <YAS>  
A:Cross-references: DDBJ:D38103; NID:9644880; PIDN:BAA07284.1; PID:g765087  
C:Superfamily: glucagon receptor  
C:Keywords: receptor; transmembrane protein  
F:136-157/Domain: transmembrane #status predicted <TM1>  
F:167-186/Domain: transmembrane #status predicted <TM2>  
F:215-238/Domain: transmembrane #status predicted <TM3>  
F:252-274/Domain: transmembrane #status predicted <TM4>  
F:292-315/Domain: transmembrane #status predicted <TM5>  
F:339-357/Domain: transmembrane #status predicted <TM6>  
F:383-394/Domain: transmembrane #status predicted <TM7>

Query Match 2.4%; Score 13; DB 2; Length 462;  
Best Local Similarity 100.0%; Pred. No. 7.7e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNYIHM 181  
|||||  
Db 159 FRLHCTRNYIHM 171

RESULT 13  
JC2195  
vasoactive intestinal peptide receptor-related protein precursor (clone hIVR5) - huma  
C:Species: Homo sapiens (man)  
C:Date: 28-Aug-1995 #sequence\_revision 07-Oct-1994 #text\_change 24-Nov-1999  
C:Accession: JC2195; S42087  
R:Couvineau, A.; Rouyer-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-De  
Biochem. Biophys. Res. Commun. 200, 769-776, 1994  
A:Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA  
A:Reference number: JC2194; MUID:94235025  
A:Accession: JC2195  
A:Molecule type: mRNA  
A:Residues: 1-495 <COU>  
A:Cross-references: EMBL:X77777; NID:9456352; PIDN:CAA54814.1; PID:9456353  
A:Experimental source: jejunal epithelial cell  
C:Genetics:  
A:Gene: GDB:VIPR1; RCD1; HVRI  
A:Cross-references: GDB:128589; OMIM:192321  
A:Map position: 3p22-3p22  
C:Superfamily: glucagon receptor  
C:Keywords: glycoprotein; intestine; phosphoprotein; receptor; transmembrane protein  
F:1-31/Domain: signal sequence #status predicted <SIG>  
F:32-495/Product: vasoactive intestinal peptide receptor-related protein #status pred  
F:180-203/Domain: transmembrane #status predicted <TM1>  
F:211-229/Domain: transmembrane #status predicted <TM2>  
F:251-269/Domain: transmembrane #status predicted <TM3>  
F:290-312/Domain: transmembrane #status predicted <TM4>  
F:334-354/Domain: transmembrane #status predicted <TM5>  
F:381-398/Domain: transmembrane #status predicted <TM6>  
F:412-431/Domain: transmembrane #status predicted <TM7>  
F:93,104,135,328/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:111/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicte  
F:285/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicte  
F:485/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicte

Query Match 2.4%; Score 13; DB 2; Length 495;  
Best Local Similarity 100.0%; Pred. No. 8.2e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHMLF 184  
|||||  
Db 205 LHCTRNYIHMLF 217

## RESULT 14

G02234  
gastric inhibitory polypeptide receptor - human  
N:Alternate names: GIP receptor  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 24-Sep-1999  
C:Accession: G02234  
R:Bonner, T.I.; Usdin, T.B.  
submitted to the EMBL Data Library, October 1995  
A:Reference number: G09336  
A:Accession: G02234  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-466 <BON>  
A:Cross-references: EMBL:U39231; NID:g1066050; PIDN:AAA84418.1; PID:g1066051  
C:Genetics:  
A:Gene: GDB:GIPR  
A:Cross-references: GDB:335023  
A:Map position: 19q13.3-19q13.3  
C:Superfamily: glucagon receptor

Query Match 2.2%; Score 12; DB 2; Length 466;  
Best Local Similarity 100.0%; Pred. No. 0.00082;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRLHCTRNYYH 180  
|||||

Db 162 FRLHCTRNYYH 173

## RESULT 15

S66676  
glucose-dependent insulintropic protein receptor precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
C:Accession: S66676  
R:Volz, A.; Goeke, R.; Lankat-Buttigereit, B.; Fehmann, H.C.; Bode, H.P.; Goeke, B.  
FEBS Lett. 373, 23-29, 1995  
A:Title: Molecular cloning, functional expression, and signal transduction of the GIP-receptor  
A:Reference number: S66676; MUID:96013879  
A:Accession: S66676  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-466 <VOL>  
A:Cross-references: GB:S79852  
A:Note: the authors translated the codon GCC for residue 427 as Leu  
C:Superfamily: glucagon receptor  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-466/Product: glucose-dependent insulintropic protein receptor #status predicted <V

Query Match 2.2%; Score 12; DB 2; Length 466;  
Best Local Similarity 100.0%; Pred. No. 0.00082;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRLHCTRNYYH 180  
|||||

Db 162 FRLHCTRNYYH 173

## RESULT 16

I37411  
glucose-dependent insulintropic polypeptide receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 24-Sep-1999  
C:Accession: I37411  
R:Gremlich, S.; Porret, A.; Hani, E.H.; Cherif, D.; Vionnet, N.; Froguel, P.; Thorens, B.  
Diabetes 44, 1202-1208, 1995  
A:Title: Cloning, functional expression, and chromosomal localization of the human pancreatic islet 1 gene  
A:Reference number: I37411; MUID:96007224  
A:Accession: I37411

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-491 <RES>  
A:Cross-references: EMBL:X81832; NID:g1030050; PIDN:CAA57426.1; PID:g1030051  
C:Superfamily: glucagon receptor

Query Match 2.2%; Score 12; DB 2; Length 491;  
Best Local Similarity 100.0%; Pred. No. 0.00085;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRLHCTRNYYH 180  
|||||

Db 161 FRLHCTRNYYH 172

## RESULT 17

JC2041  
glucagon receptor precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 28-May-1999  
C:Accession: JC2041  
R:MacNeil, D.J.; Occi, J.L.; Hey, P.J.; Strader, C.D.; Graziano, M.P.  
Biochem. Biophys. Res. Commun. 198, 328-334, 1994  
A:Title: Cloning and expression of a human glucagon receptor.  
A:Reference number: JC2041; MUID:94121651  
A:Accession: JC2041  
A:Molecule type: mRNA  
A:Residues: 1-477 <MAC>  
A:Cross-references: GB:U03469; NID:g439689; PIDN:AAC52063.1; PID:g439690  
C:Genetics:  
A:Gene: GDB:GGR; GGR

A:Cross-references: GDB:304516; OMIM:138033  
A:Map position: 17q25-17q25  
C:Superfamily: glucagon receptor  
C:Keywords: glycoprotein; receptor; transmembrane protein  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-477/Product: glucagon receptor #status predicted <MAT>  
F:143-166/Domain: transmembrane #status predicted <TM1>  
F:174-194/Domain: transmembrane #status predicted <TM2>  
F:226-244/Domain: transmembrane #status predicted <TM3>  
F:266-285/Domain: transmembrane #status predicted <TM4>  
F:302-323/Domain: transmembrane #status predicted <TM5>  
F:352-369/Domain: transmembrane #status predicted <TM6>  
F:386-403/Domain: transmembrane #status predicted <TM7>  
F:46,59,74,78/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.8%; Score 10; DB 2; Length 477;  
Best Local Similarity 100.0%; Pred. No. 0.093;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 LVEGLYLHNL 264  
|||||

Db 243 LVEGLYLHNL 252

Search completed: September 21, 2001, 17:10:40  
Job time: 128 sec

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OM protein - protein search, using sw model

Run on: September 21, 2001, 17:09:57 ; Search time 13.32 Seconds  
(without alignments)  
1391.308 Million cell updates/sec

Title: US-09-236-468A-2  
Perfect score: 541  
Sequence: 1 MAWLGLASLHWGWLMLGSL.....DDILMEKPSRPMSNPDETEG 541

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size : 10

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	363	67.1	550	1 PTH2_HUMAN	P49190 homo sapien
2	33	6.1	546	1 PTH2_RAT	P70555 rattus norv
3	25	4.6	585	1 PTH2_DIDNA	P25107 didelphis m
4	19	3.5	440	1 SCRC_HUMAN	P47872 homo sapien
5	19	3.5	449	1 SCRC_RAT	P23811 rattus norv
6	18	3.3	585	1 PTH2_PIG	P50133 sus scrofa
7	18	3.3	591	1 PTH2_MOUSE	P41593 mus musculu
8	18	3.3	591	1 PTH2_RAT	P25961 rattus norv
9	18	3.3	593	1 PTH2_HUMAN	Q03431 homo sapien
10	16	3.0	445	1 SCRC_RABIT	O46502 oryctolagus
11	16	3.0	447	1 VIPR_CARAU	Q90308 carassius a
12	13	2.4	455	1 GIPR_RAT	P43219 rattus norv
13	13	2.4	457	1 VIPR_HUMAN	P32241 homo sapien
14	13	2.4	458	1 VIPR_PIG	Q28992 sus scrofa
15	13	2.4	459	1 GIPR_RAT	P30083 rattus norv
16	13	2.4	462	1 GIPR_MESAU	P43218 mesocricetu
17	12	2.2	466	1 GIPR_HUMAN	P48546 homo sapien
18	10	1.8	477	1 GIPR_HUMAN	P47871 homo sapien
19	10	1.8	550	1 GLP2_RAT	Q920W0 rattus norv
20	10	1.8	553	1 GLP2_HUMAN	O95838 homo sapien

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	550 AA.
PTH2_HUMAN				
AC	P49190;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	PARATHYROID HORMONE RECEPTOR PRECURSOR (PTH2 RECEPTOR).			

GN PTH2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
RC TISSUE=Brain;  
RX MEDLINE=95318121; PubMed=7797535;  
RA Usdin T.B., Gruber C., Bonner T.I.;  
RT "Identification and functional expression of a receptor selectively  
recognizing parathyroid hormone, the PTH2 receptor.";  
RL J. Biol. Chem. 270:15455-15458(1995).  
RN [2]  
RP SEQUENCE OF 26-40 AND 306-550 FROM N.A.  
RX MEDLINE=97079671; PubMed=8921382;  
RA Usdin T.B., Modi W., Bonner T.I.;  
RT "Assignment of the human PTH2 receptor gene (PTH2) to chromosome 2q33  
by fluorescence in situ hybridization.";  
RL Genomics 37:140-141(1996).  
CC -!- FUNCTION: THIS IS A SPECIFIC RECEPTOR FOR PARATHYROID HORMONE. THE  
ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE  
ADENYL CYCLASE.  
CC -!- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN BRAIN AND PANCREAS.  
CC ALSO EXPRESSED IN THE TESTIS.  
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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or send an email to license@isb-sib.ch).  
CC  
DR EMBL; U25128; AAC50157.1; -;  
DR EMBL; U47124; AAC96796.1; -;  
DR EMBL; U47129; AAC50767.1; -;  
DR EMBL; U47125; AAC50767.1; JOINED.  
DR EMBL; U47126; AAC50767.1; JOINED.  
DR EMBL; U47127; AAC50767.1; JOINED.  
DR EMBL; U47128; AAC50767.1; JOINED.  
DR GCRDb; GCR\_2003; -;  
DR MIM; 601469; -;  
DR InterPro; IPR000832; -;  
DR Pfam; PF00002; 7tm2; 1.  
DR PRINTS; PR00249; GPCRSECRETIN.  
DR PROSITE; PS00649; G\_PROTEIN\_RECP\_F2\_1; 1.  
DR PROSITE; PS00500; G\_PROTEIN\_RECP\_F2\_2; 1.  
DR PROSITE; PS00527; G\_PROTEIN\_RECP\_F2\_3; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 550  
FT DOMAIN 27 145  
FT TRANSMEM 146 169  
FT DOMAIN 170 176  
FT TRANSMEM 177 196  
FT DOMAIN 197 237  
FT TRANSMEM 238 260  
FT DOMAIN 261 275  
FT TRANSMEM 276 297  
FT DOMAIN 298 316  
FT TRANSMEM 317 337  
FT DOMAIN 338 364  
FT TRANSMEM 365 383  
FT DOMAIN 384 394  
FT TRANSMEM 395 417  
FT DOMAIN 418 550  
FT CARBOHYD 51 51  
FT CARBOHYD 106 106  
FT CARBOHYD 116 116  
FT CARBOHYD 121 121  
SQ SEQUENCE 550 AA; 62235 MW; 2ADD14DBA68A9BF8 CRC64;

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Query Match          67.1%; Score 363; DB 1; Length 550;
Best Local Similarity 99.8%; Pred No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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CC -----
DR EMBL; U5836; AAC52849.1; -
DR GCRdb; GCR_1413; -
DR InterPro; IPR000832; -
DR Pfam; PF00002; 7tm.2; 1
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
DR PROSITE; PS00651; G_PROTEIN_RECEP_F2_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24 POTENTIAL
FT CHAIN 25 546 PARATHYROID HORMONE RECEPTOR.
FT DOMAIN 27 143 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 144 167 1 (POTENTIAL).
FT DOMAIN 168 174 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 175 194 2 (POTENTIAL).
FT DOMAIN 195 235 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 236 258 3 (POTENTIAL).
FT DOMAIN 259 273 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 274 295 4 (POTENTIAL).
FT DOMAIN 296 313 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 314 334 5 (POTENTIAL).
FT DOMAIN 335 361 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 362 380 6 (POTENTIAL).
FT DOMAIN 381 391 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 392 414 7 (POTENTIAL).
FT DOMAIN 415 546 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 546 AA; 61800 MW; 2825AE4040313527 CRC64;

Query Match          6.1%; Score 33; DB 1; Length 546;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 YTVGYSISFGSLAVAILIIGYFRRHLCTRNYIH 180
DB 146 YTVGYSISFGSLAVAILIIGYFRRHLCTRNYIH 178

RESULT 3
PTHR_DIDMA
ID PTHR_DIDMA STANDARD; PRT; 585 AA.
AC P25107;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
GN PRECURSOR (PTH/PTHr RECEPTOR).
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92054592; PubMed=1658941;
RA Jueppner H., Abou-Samra A.-B., Freeman M., Kong X.-F., Schipani E.,
RA Richards J., Koliakowski L.F. Jr., Hock J., Potts J.T. Jr.,
RA Kronenberg H.M., Segre G.V.;
RT "A G protein-linked receptor for parathyroid hormone and parathyroid
RT hormone-related peptide."
RL Science 254:1024-1026(1991).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
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FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 124 124 G -> A (IN REF. 1).
FT CONFLICT 210 210 A -> P (IN REF. 2).
FT CONFLICT 308 308 I -> F (IN REF. 3).
FT CONFLICT 333 333 E -> Q (IN REF. 3).
FT CONFLICT 377 377 G -> A (IN REF. 1).
SQ SEQUENCE 440 AA; 50206 MW; E22CDD0EE7C0ACC1 CRC64;

Query Match 3.5%; Score 19; DB 1; Length 440;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNHYIHMHLFVSF 187
IIIIIIIIIIIIIIIIIIII
DB 167 FRLHCTRNHYIHMHLFVSF 185

RESULT 5
SCRC_RAT STANDARD; PRT; 449 AA.
AC P2381I;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE SECRETIN RECEPTOR PRECURSOR (SCT-R).
GN SCTR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP MEDLINE=91266890; PubMed=1646711;
RA Ishihara T., Nakamura S., Kaziro Y., Takahashi T., Takahashi K.,
RA Nagata S.;
RT "Molecular cloning and expression of a cDNA encoding the secretin
RT receptor.";
RL EMBO J. 10:1635-1641(1991).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL; X59132; CAA41849.1; -.
CC DR PIR; S16319; S16319.
CC DR GCRdb; GCR_0242; -.
CC DR InterPro; IPR000832; -.
CC DR Pfam; PF00002; 7tm2; 1.
CC DR PRINTS; PR00249; GPCRSECRETIN.
CC DR PROSITE; PS00649; G_PROTEIN_RECP_F2.1; 1.
CC DR PROSITE; PS00650; G_PROTEIN_RECP_F2.2; 1.
CC DR PROSITE; PS0227; G_PROTEIN_RECP_F2.3; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
KW SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 449 SECRETIN RECEPTOR.
FT DOMAIN 23 143 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 144 167 1 (POTENTIAL).
FT DOMAIN 168 174 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 175 194 2 (POTENTIAL).
FT DOMAIN 195 216 EXTRACELLULAR (POTENTIAL).
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FT TRANSMEM 217 240 3 (POTENTIAL).
FT DOMAIN 241 254 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 255 276 4 (POTENTIAL).
FT DOMAIN 277 294 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 317 5 (POTENTIAL).
FT DOMAIN 318 343 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 344 362 6 (POTENTIAL).
FT TRANSMEM 363 392 7 (POTENTIAL).
FT DOMAIN 393 449 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 449 AA; 51234 MW; E70D05B5D061480D CRC64;

Query Match 3.5%; Score 19; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 2.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNHYIHMHLFVSF 187
IIIIIIIIIIIIIIIIIIII
DB 167 FRLHCTRNHYIHMHLFVSF 185

RESULT 6
PRR_PIG STANDARD; PRT; 585 AA.
ID PTHR_PIG
AC P50133;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
DE PRECURSOR (PTHr/PTHr RECEPTOR).
GN PTHRI OR PTHR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96303558; PubMed=8688470;
RA Black E.C., Smith D.P., Zhang X.Y., Frolik C.A., Harvey A.,
RA Chandrasekhar S., Hsiung H.M.;
RT "Structure and functional expression of a complementary DNA for
RT porcine parathyroid hormone/parathyroid hormone-related peptide
RT receptor.";
RL Biochim. Biophys. Acta 1307:339-347(1996).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC SYSTEM (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC -----
CC EMBL; U18315; AAC48619.1; -.
CC DR GCRdb; GCR_1607; -.
CC DR InterPro; IPR000832; -.
CC DR Pfam; PF00002; 7tm2; 1.
CC DR PRINTS; PR00249; GPCRSECRETIN.
CC DR PRINTS; PR00393; PTHRMONER.
```

DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
DR PROSITE; PS0227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 26  
FT CHAIN 27 585  
FT DOMAIN 27 184  
FT TRANSMEM 185 208  
FT DOMAIN 209 215  
FT TRANSMEM 216 235  
FT DOMAIN 236 277  
FT TRANSMEM 278 301  
FT DOMAIN 302 315  
FT TRANSMEM 316 337  
FT DOMAIN 338 356  
FT TRANSMEM 357 377  
FT DOMAIN 378 404  
FT TRANSMEM 405 423  
FT DOMAIN 424 435  
FT TRANSMEM 436 458  
FT DOMAIN 459 585  
FT CARBOHYD 147 147  
FT CARBOHYD 157 157  
FT CARBOHYD 162 162  
FT CARBOHYD 172 172  
SQ SEQUENCE 585 AA; 65682 MW; 60BE15CD49B7D210 CRC64;

Query Match 3.3%; Score 18; DB 1; Length 585;  
Best Local Similarity 100.0%; Pred. No. 2.8e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 245 YFLATNYWILVEGLYLH 262  
Db 285 YFLATNYWILVEGLYLH 302

RESULT 7  
PTRR\_MOUSE STANDARD; PRT; 591 AA.  
AC P41593; Q62119;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR  
DE PRECURSOR (PTH/PTRH RECEPTOR).  
GN PTHRI OR PTRH.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=C3H/HEHA;  
RC MEDLINE=95034305; PubMed=7524627;  
RA Karperien M., van Dijk T.B., Hoelmakers T., Cremers F.,  
RA Abou-Samra A.-B., Boonstra J., de Laat S.W., Defize L.H.K.;  
RT "Expression pattern of parathyroid hormone/parathyroid hormone  
RT related peptide receptor mRNA in mouse postimplantation embryos  
RT indicates involvement in multiple developmental processes.";  
RN Mech. Dev. 47:29-42(1994).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RX MEDLINE=94255468; PubMed=8197183;  
RA McCuaig K.A., Clarke J.C., White J.H.;  
RT "Molecular cloning of the gene encoding the mouse parathyroid  
RT hormone/parathyroid hormone-related peptide receptor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:5051-5055(1994).  
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR  
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS  
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL

CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER  
CC SYSTEM.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
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CC -----  
DR EMBL; X78936; CAA5536.1; -  
DR EMBL; L34611; AAA4001.1; -  
DR EMBL; L34608; AAA4001.1; JOINED.  
DR EMBL; L34607; AAA4001.1; JOINED.  
DR EMBL; L34609; AAA4001.1; JOINED.  
DR EMBL; L34610; AAA4001.1; JOINED.  
DR GCRDB; GCR\_1005; -  
DR GCRDB; GCR\_1614; -  
DR MGD; MGI:97801; Pthr.  
DR InterPro; IPR000832; -  
DR InterPro; IPR002170; -  
DR Pfam; PF00002; 7tm2; 1.  
DR PRINTS; PR00249; GPCRSECRETIN.  
DR PRINTS; PR00393; PTRHORMONER.  
DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
DR PROSITE; PS0227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 26  
FT CHAIN 27 591  
FT DOMAIN 27 188  
FT TRANSMEM 189 212  
FT DOMAIN 214 219  
FT TRANSMEM 220 239  
FT DOMAIN 240 282  
FT TRANSMEM 283 306  
FT DOMAIN 307 320  
FT TRANSMEM 321 342  
FT DOMAIN 343 361  
FT TRANSMEM 362 382  
FT DOMAIN 383 409  
FT TRANSMEM 410 428  
FT DOMAIN 429 440  
FT TRANSMEM 441 463  
FT DOMAIN 464 591  
FT CARBOHYD 151 151  
FT CARBOHYD 161 161  
FT CARBOHYD 166 166  
FT CARBOHYD 176 176  
FT CARBOHYD 27 28  
FT CONFLICT 464 465  
FT CONFLICT 500 501  
SQ SEQUENCE 591 AA; 66313 MW; F7876F8D388BDDFD CRC64;

Query Match 3.3%; Score 18; DB 1; Length 591;  
Best Local Similarity 100.0%; Pred. No. 2.8e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 245 YFLATNYWILVEGLYLH 262  
Db 290 YFLATNYWILVEGLYLH 307

RESULT 8  
PTRR\_RAT STANDARD; PRT; 591 AA.  
ID PTRR\_RAT  
AC P25961;  
DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR  
 DE PRECURSOR (PTH/PTHr RECEPTOR).  
 GN PTHR1 OR PTHR.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Bone;  
 RC MEDLINE=92212903; PubMed=1313566;  
 RX Abou-Samra A.-B., Jueppner H., Force T., Freeman M.W., Kong X.-F.,  
 RA Schipani E., Urena P., Richards J., Bonventre J.V., Potts J.T. Jr.,  
 RA Kronenberg H.M., Segre G.V.;  
 RT "Expression cloning of a common receptor for parathyroid hormone and  
 RT parathyroid hormone-related peptide from rat osteoblast-like cells: a  
 RT single receptor stimulates intracellular accumulation of both cAMP  
 RT and inositol trisphosphates and increases intracellular free  
 RT calcium.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2732-2736(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94292182; PubMed=8020952;  
 RA Fausova Z., Bourdon J., Clayton D., Mattel M.-G., Seldin M.F.,  
 RA Janicic N., Riviere M., Szpirer J., Levan G., Szpirer C.;  
 RT "Cloning of a parathyroid hormone/parathyroid hormone-related peptide  
 RT receptor (PTHr) cDNA from a rat osteosarcoma (UMR 106) cell line:  
 RT chromosomal assignment of the gene in the human, mouse, and rat  
 RT genomes.";  
 RL Genomics 20:20-26(1994).  
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR  
 CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS  
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL  
 CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER  
 CC SYSTEM.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL; W7184; AAA1811.1; -;  
 DR EMBL; L19475; AAA68098.1; -;  
 DR GCRDB; GCR\_0206; -;  
 DR GCRDB; GCR\_0938; -;  
 DR InterPro; IPR000832; -;  
 DR InterPro; IPR002170; -;  
 DR Pfam; PF00002; 7tm2; 1.  
 DR PRINTS; PR00249; GPCRSECRETIN.  
 DR PRINTS; PR00393; PTRHORMONER.  
 DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
 DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
 DR PROSITE; PS50227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 26  
 FT CHAIN 27 591  
 FT PARATHYROID HORMONE/PARATHYROID HORMONE-  
 FT RELATED PEPTIDE RECEPTOR.  
 FT DOMAIN 27 188  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 189 212  
 FT DOMAIN 214 219  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 220 239  
 FT DOMAIN 240 282  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 283 306  
 FT DOMAIN 307 320  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 321 342  
 FT DOMAIN 343 361  
 FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 362 382  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 383 409  
 FT TRANSMEM 410 428  
 FT DOMAIN 429 440  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 441 463  
 FT DOMAIN 464 591  
 FT CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 151 151  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 161 161  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 166 166  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 176 176  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 591 AA; 66260 MW; 21944F3051B9E9C1 CRC64;  
 Query Match 3.3%; Score 18; DB 1; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 245 YFLATNYWILVEGLYLH 262  
 |||||  
 DB 290 YFLATNYWILVEGLYLH 307  
 |||||  
 RESULT 9  
 PTRR\_HUMAN STANDARD; PRT; 593 AA.  
 ID AC Q03431;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR  
 DE PRECURSOR (PTH/PTHr RECEPTOR).  
 GN PTHR1 OR PTHR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=9338641; PubMed=8386612;  
 RA Schipani E., Karga H., Karaplis A.C., Potts J.T. Jr., Kronenberg H.M.,  
 RA Abou-Samra A.-B., Segre G.V., Jueppner H.;  
 RT "Identical complementary deoxyribonucleic acids encode a human renal  
 RT and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";  
 RL Endocrinology 132:2157-2165(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=93387403; PubMed=8397094;  
 RA Schneider H., Feyen J.-H., Rao Movva N.;  
 RT "Cloning and functional expression of a human parathyroid hormone  
 RT receptor.";  
 RL Eur. J. Pharmacol. 246:149-155(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95263723; PubMed=7745008;  
 RA Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.F.,  
 RA Stuhmann M., Kruse K., Whyte M.P., Murray T., Schmidtke J., Dop C.,  
 RA Brickman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M.,  
 RA Abou-Samra A.-B., Segre G.V., Jueppner H.;  
 RT "pseudohypoparathyroidism type 1b is not caused by mutations in the  
 RT coding exons of the human parathyroid hormone (PTH)/PTH-related  
 RT peptide receptor gene.";  
 RL J. Clin. Endocrinol. Metab. 80:1611-1621(1995).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Levine M.A.;  
 RL Submitted (xxx-1995) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP STRUCTURE BY NMR OF 168-198.  
 RX MEDLINE=98409426; PubMed=9737850;  
 RA Pellegrini M., Bisello A., Rosenblatt M., Chorev M., Mierke D.F.;



```
RT "Molecular cloning and in vitro properties of the recombinant rabbit
RL secretin receptor.";
CC Peptides 19:1055-1062(1998).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF025411; AAC32767.1; -.
CC InterPro: IPR000832; -.
CC InterPro: IPR001771; -.
CC Pfam: PF0002144; -.
CC PRINTS: PR00249; GPCRSECRETIN.
CC PRINTS: PR00490; SECRETINR.
CC PRINTS: PRO1134; VIPRECEPTOR.
CC PROSITE: PS00649; G-PROTEIN_RECEP_F2_1; 1.
CC PROSITE: PS00650; G-PROTEIN_RECEP_F2_2; 1.
CC PROSITE: PS00651; G-PROTEIN_RECEP_F2_3; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 445
FT DOMAIN 22 139
FT TRANSMEM 140 163
FT DOMAIN 164 170
FT TRANSMEM 171 190
FT DOMAIN 191 212
FT TRANSMEM 213 236
FT DOMAIN 237 250
FT TRANSMEM 251 272
FT DOMAIN 273 290
FT TRANSMEM 291 313
FT DOMAIN 314 339
FT TRANSMEM 340 358
FT DOMAIN 359 365
FT TRANSMEM 366 388
FT DOMAIN 389 445
FT CARBOHYD 68 68
FT CARBOHYD 96 96
FT CARBOHYD 102 102
FT CARBOHYD 124 124
FT SEQUENCE 445 AA; 50495 MW; 31C4169CB099F194 CRC64;
SQ
Query Match 3.0%; Score 16; DB 1; Length 445;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 169 FRLHCTRNVIHMLF 184
Db 163 FRLHCTRNVIHMLF 178
|||||
RESULT 11
VIPR_CARAU
ID VIPR_CARAU STANDARD; PRT; 447 AA.
AC Q90308;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR (VIP-R) (VIP RECEPTOR).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
```

```
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
RN NCBI_TaxID=7957;
RX SEQUENCE FROM N.A.
RX MEDLINE=97190233; PubMed=9038250;
RA Chow B.K.C., Yuen T.T.H., Chan K.W.;
RT "Molecular evolution of vertebrate VIP receptors and functional
RT characterization of a VIP receptor from goldfish Carassius auratus.";
RL Gen. Comp. Endocrinol. 105:176-185(1997).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U56391; AAB05459.1; -.
CC GCRDb; GCR_1205; -.
CC InterPro; IPR000832; -.
CC Pfam; PF00002; 7tm.2; 1.
CC PRINTS: PR00249; GPCRSECRETIN.
CC PROSITE: PS00649; G-PROTEIN_RECEP_F2_1; 1.
CC PROSITE: PS00650; G-PROTEIN_RECEP_F2_2; 1.
CC PROSITE: PS00651; G-PROTEIN_RECEP_F2_3; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 103
FT TRANSMEM 104 128
FT DOMAIN 129 135
FT TRANSMEM 136 155
FT DOMAIN 156 178
FT TRANSMEM 179 202
FT DOMAIN 203 216
FT TRANSMEM 217 238
FT DOMAIN 239 255
FT TRANSMEM 257 280
FT DOMAIN 281 305
FT TRANSMEM 306 325
FT DOMAIN 326 337
FT TRANSMEM 338 357
FT DOMAIN 358 447
FT CARBOHYD 17 17
FT CARBOHYD 22 22
FT CARBOHYD 64 64
FT CARBOHYD 91 91
FT CARBOHYD 169 169
FT SEQUENCE 447 AA; 50959 MW; 66839E243702554C CRC64;
SQ
Query Match 3.0%; Score 16; DB 1; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 172 LHCTRNVIHMLFVSF 187
Db 131 LHCTRNVIHMLFVSF 146
|||||
RESULT 12
GIPR_RAT
ID GIPR_RAT STANDARD; PRT; 455 AA.
AC P43219;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR PRECURSOR (GIP-R) (GLUCOSE-
DE DEPENDENT INSULINOTROPIC POLYPEPTIDE RECEPTOR).
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GN OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;  
RX MEDLINE=94062667; PubMed=8243312;  
RA Usdin T.B., Mezey E., Button D.C., Brownstein M.J., Bonner T.I.;  
RT "Gastric inhibitory polypeptide receptor, a member of the secretin-  
RT vasoactive intestinal peptide receptor family, is widely distributed  
RT in peripheral organs and the brain.";  
RL Endocrinology 133:2861-2871(1993).  
CC -!- FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS  
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL  
CC CYCLASE.  
CC  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC  
CC -!- TISSUE SPECIFICITY: PRESENT IN THE PANCREAS AS WELL AS THE GUT,  
CC ADIPOSE TISSUE, HEART, PITUITARY, AND INNER LAYERS OF THE ADRENAL  
CC CORTEX, WHEREAS IT IS NOT FOUND IN KIDNEY, SPLEEN, OR LIVER. IT IS  
CC ALSO EXPRESSED IN SEVERAL BRAIN REGIONS, INCLUDING THE CEREBRAL  
CC CORTEX, HIPPOCAMPUS, AND OLFACTORY BULB.  
CC  
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
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CC  
CC EMBL: L19660; AAC37637.1; -  
CC CCRdb; GCR\_0817; -  
DR InterPro; IPR000832; -  
DR InterPro; IPR001749; -  
DR Pfam; PF00002; 7tm\_2; 1.  
DR PRINTS; PR00249; GPCRSECRETIN.  
DR PRINTS; PR01129; GIPRECEPTOR.  
DR PROSITE; PS00649; G\_PROTEIN\_RECP\_F2\_1; 1.  
DR PROSITE; PS00650; G\_PROTEIN\_RECP\_F2\_2; 1.  
DR PROSITE; PS00627; G\_PROTEIN\_RECP\_F2\_3; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 18  
FT CHAIN 19 455  
FT DOMAIN 19 135  
FT TRANSMEM 136 158  
FT DOMAIN 159 166  
FT TRANSMEM 167 186  
FT DOMAIN 187 214  
FT TRANSMEM 215 239  
FT DOMAIN 240 251  
FT TRANSMEM 252 275  
FT DOMAIN 276 290  
FT TRANSMEM 291 316  
FT DOMAIN 317 338  
FT TRANSMEM 339 359  
FT DOMAIN 360 374  
FT TRANSMEM 375 395  
FT DOMAIN 396 455  
FT CARBOHYD 59 59  
FT CARBOHYD 69 69  
FT CARBOHYD 74 74  
SQ SEQUENCE 455 AA; 52256 MW; 5454B0638ABF9A06 CRC64;

Query Match 2.4%; Score 13; DB 1; Length 455;  
Best Local Similarity 100.0%; Pred. No. 3.le-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 169 FRRLHCTRYNIHM 181  
|||||||

DB 159 FRRLHCTRYNIHM 171  
RESULT 13  
VIPR\_HUMAN  
ID VIPR\_HUMAN STANDARD; PRT; 457 AA.  
AC P32241; Q15871;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1)  
DE (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR)  
DE (PACAP TYPE II RECEPTOR) (PACAP-R-2).  
GN VIPRI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Intestine;  
RX MEDLINE=93290641; PubMed=8390245;  
RA Sreedharan S.P., Patel D.R., Huang J.-X., Goetzl E.J.;  
RT "Cloning and functional expression of a human neuroendocrine  
RT vasoactive intestinal peptide receptor.";  
RL Biochem. Biophys. Res. Commun. 193:546-553(1993).  
RN [2]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RC TISSUE=Intestine;  
RX MEDLINE=94235025; PubMed=8179610;  
RA Couvineau A., Rouyer-Fessard C., Darmoul D., Maoret J.J., Carrero I.,  
RA Ogier-Denis E., Laburthe M.;  
RT "Human intestinal VIP receptor: cloning and functional expression of  
RT two cDNA encoding proteins with different N-terminal domains.";  
RL Biochem. Biophys. Res. Commun. 200:769-776(1994).  
RN [3]  
RP SEQUENCE OF 33-457 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=95001220; PubMed=7917790;  
RA Gagnon A.W., Aiyar N., Elshourbagy N.A.;  
RT "Molecular cloning and functional characterization of a human liver  
RT vasoactive intestinal peptide receptor.";  
RL Cell. Signal. 6:321-333(1994).  
CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS  
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL  
CC CYCLASE. THE AFFINITY IS VIP = PACAP-27 > PACAP-38.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE  
CC SPLICING.  
CC -!- TISSUE SPECIFICITY: IN LUNG, HT29 COLONIC EPITHELIAL CELLS,  
CC RAJI B-LYMPHOBLASTS. LESSER EXTENT IN BRAIN, HEART, KIDNEY,  
CC LIVER AND PLACENTA.  
CC  
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC  
CC EMBL: U11087; AAB60362.1; -  
DR EMBL; U11079; AAB60362.1; JOINED.  
DR EMBL; U11080; AAB60362.1; JOINED.  
DR EMBL; U11081; AAB60362.1; JOINED.  
DR EMBL; U11083; AAB60362.1; JOINED.  
DR EMBL; U11084; AAB60362.1; JOINED.  
DR EMBL; U11085; AAB60362.1; JOINED.  
DR EMBL; U11086; AAB60362.1; JOINED.  
DR EMBL; L13288; AAA36805.1; -  
DR EMBL; X77777; CAA54814.1; -  
DR EMBL; X75299; CAA53046.1; -

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DR EMBL; L20295; AAA36802.1; -.
DR PIR; JN0604; JN0604.
DR GCRDB; GCR_0397; -.
DR GCRDB; GCR_0652; -.
DR GCRDB; GCR_0774; -.
DR GCRDB; GCR_0904; -.
DR GCRDB; GCR_1888; -.
DR MIM; 192321; -.
DR InterPro; IPR000832; -.
DR InterPro; IPR001571; -.
DR InterPro; IPR001771; -.
DR Pfam; PF00002; 7tm2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRINTS; PR00491; VASOACTIVEIPR.
DR PRINTS; PR01154; VIPRECEPTOR.
DR PROSITE; PS00649; G_PROTEIN_RECF_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECF_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECF_F2_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Alternative splicing.
FT SIGNAL 1 30
FT CHAIN 31 457
FT VASOACTIVE INTESTINAL POLYPEPTIDE
FT RECEPTOR 1.
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 31 142
FT TRANSMEM 143 167
FT DOMAIN 168 174
FT TRANSMEM 175 194
FT DOMAIN 195 216
FT TRANSMEM 217 240
FT DOMAIN 241 254
FT TRANSMEM 255 276
FT DOMAIN 277 292
FT TRANSMEM 293 316
FT DOMAIN 317 341
FT TRANSMEM 342 361
FT DOMAIN 362 373
FT TRANSMEM 374 393
FT DOMAIN 394 457
FT CYTOPLASMIC (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 58 58
FT CARBOHYD 69 69
FT CARBOHYD 100 100
FT CARBOHYD 290 290
FT VARSPPLIC 1 32
FT SEQUENCE 457 AA; 51547 MW; DAA40CF5BEC47D7D CRC64;

Query Match 2.4%; Score 13; DB 1; Length 457;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHMLF 184
Db 170 LHCTRNVIHMLF 182
|||||

RESULT 14
VIPR_PIG STANDARD; PRT; 458 AA.
AC Q28992;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR I PRECURSOR (VIP-R-1)
DE (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR)
DE (PACAP TYPE II RECEPTOR) (PACAP-R-2).
GN VIPRL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
```

SEQUENCE FROM N.A.  
Hsiung H.M., Smith D.P., Hyslop P.A., Helman M.L., Hassan H.A.,  
Zhang X.;  
Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS  
RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL  
CYCLASE (BY SIMILARITY).  
!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
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-----  
EMBL; U49434; AAA93390.1; -.  
GCRDB; GCR\_1565; -.  
InterPro; IPR000832; -.  
InterPro; IPR001571; -.  
InterPro; IPR001771; -.  
Pfam; PF00002; 7tm2; 1.  
PRINTS; PR00249; GPCRSECRETIN.  
PRINTS; PR00491; VASOACTIVEIPR.  
PRINTS; PR01154; VIPRECEPTOR.  
PROSITE; PS00649; G\_PROTEIN\_RECF\_F2\_1; 1.  
PROSITE; PS00650; G\_PROTEIN\_RECF\_F2\_2; 1.  
PROSITE; PS00227; G\_PROTEIN\_RECF\_F2\_3; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 31  
FT CHAIN 32 458  
FT VASOACTIVE INTESTINAL POLYPEPTIDE  
FT RECEPTOR 1.  
FT EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 144 168  
FT DOMAIN 169 175  
FT TRANSMEM 176 195  
FT DOMAIN 196 217  
FT TRANSMEM 218 241  
FT DOMAIN 242 255  
FT TRANSMEM 256 277  
FT DOMAIN 278 293  
FT TRANSMEM 294 317  
FT DOMAIN 318 342  
FT TRANSMEM 343 362  
FT DOMAIN 363 374  
FT TRANSMEM 375 394  
FT DOMAIN 395 458  
FT CARBOHYD 59 59  
FT CARBOHYD 70 70  
FT CARBOHYD 101 101  
FT CARBOHYD 105 105  
FT SEQUENCE 458 AA; 51479 MW; E166E4D6B3BE1189 CRC64;

Query Match 2.4%; Score 13; DB 1; Length 458;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHMLF 184  
Db 171 LHCTRNVIHMLF 183  
|||||

RESULT 15  
VIPR\_RAT STANDARD; PRT; 459 AA.  
AC P30083;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR I PRECURSOR (VIP-R-1)



FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 462 AA; 52918 MW; D7A6204BCB9BB688 CRC64;

Query Match 2.4%; Score 13; DB 1; Length 462;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIHM 181  
Db 159 FRLHCTRNVIHM 171

RESULT 17  
GIPR\_HUMAN STANDARD; PRT; 466 AA.  
AC P48346; Q16400; Q14401;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR PRECURSOR (GIP-R) (GLUCOSE-DEPENDENT INSULINOTROPIC POLYPEPTIDE RECEPTOR).  
DE GIPR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Usdin T.B., Gruber C., Modi W., Bonner T.I.;  
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96013879; PubMed=7589426;  
RA Volz A., Goke R., Lankat-Buttgereit B., Fehmann H.C., Bode H.P.,  
RA Goke B.;  
RT "Molecular cloning, functional expression, and signal transduction of  
the GIP-receptor cloned from a human insulinoma.";  
RL FEBS Lett. 373:23-29(1995).  
RN [3]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX TISSUE=Pancreas;  
RX MEDLINE=96007224; PubMed=7556958;  
RA Greulich S., Porret A., Hani E.H., Cherif D., Vionnet N., Froguel P.,  
RA Thorens B.;  
RT "Cloning, functional expression, and chromosomal localization of the  
human pancreatic islet glucose-dependent insulinotropic polypeptide  
receptor.";  
RL Diabetes 44:1202-1208(1995).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96121393; PubMed=8575774;  
RA Yamada Y., Hayami T., Nakamura K., Kaisaki P.J., Someya Y.,  
RA Wang C.Z., Seino S., Seino Y.;  
RT "Human gastric inhibitory polypeptide receptor: cloning of the gene  
(GIPR) and cDNA.";  
RL Genomics 29:773-776(1995).  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,  
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,  
RA Phan H., Velasco N., Do L., Regala N., Terry A., Ganes J.,  
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,  
RA Attix C., Andreise T., Frankheim M., Amico-Keller G., Coefield J.,  
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,  
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
RA Olsen A.S., Carrano A.V.;  
RT "Sequence analysis of a 1.9 Mb region in 19q13.2 between APOE and  
DL9S412.";  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS  
RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL

CC CYCLASE.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE  
CC SPLICING.  
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; U39231; AAA84418.1; -;  
DR EMBL; S79852; AAB35419.2; -;  
DR EMBL; X81832; CAA57426.1; -;  
DR EMBL; D49559; BAA08503.1; -;  
DR EMBL; D49556; BAA08503.1; JOINED.  
DR EMBL; D49557; BAA08503.1; JOINED.  
DR EMBL; D49558; BAA08503.1; JOINED.  
DR EMBL; AC006132; AAC97984.1; -;  
DR GCRdb; GCR\_1157; -;  
DR GCRdb; GCR\_1955; -;  
DR GCRdb; GCR\_1987; -;  
DR GCRdb; GCR\_2098; -;  
DR MIM; 137241; -;  
DR InterPro; IPR000832; -;  
DR InterPro; IPR001749; -;  
DR Pfam; PF00002; 7tm\_2; 1.  
DR PRINTS; PR00249; GPCRSECRETIN.  
DR PRINTS; PR01129; GIPRECEPTOR.  
DR PROSITE; PS00649; G-PROTEIN\_RECF\_F2\_1; 1.  
DR PROSITE; PS00650; G-PROTEIN\_RECF\_F2\_2; 1.  
DR PROSITE; PS00227; G-PROTEIN\_RECF\_F2\_3; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
KW Alternative splicing.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 466 GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR.  
FT DOMAIN 22 138 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 139 161 1 (POTENTIAL).  
FT DOMAIN 162 169 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 170 189 2 (POTENTIAL).  
FT DOMAIN 190 217 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 218 242 3 (POTENTIAL).  
FT DOMAIN 243 254 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 255 278 4 (POTENTIAL).  
FT DOMAIN 279 293 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 294 319 5 (POTENTIAL).  
FT DOMAIN 320 341 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 342 362 6 (POTENTIAL).  
FT DOMAIN 363 377 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 378 398 7 (POTENTIAL).  
FT DOMAIN 399 466 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPLIC 399 399 V -> VGRDPAAPALWRRRGTPPLSAIVSQ (IN  
LONG ISOFORM).  
FT CONFLICT 12 12 R -> G (IN REF. 2).  
FT CONFLICT 104 104 G -> R (IN REF. 2).  
FT CONFLICT 117 117 MISSING (IN REF. 3).  
FT CONFLICT 337 337 L -> V (IN REF. 2).  
FT CONFLICT 367 371 GALRF -> APCV (IN REF. 3).  
FT SEQUENCE 466 AA; 53156 MW; CA5CF86BA0E32383 CRC64;  
SQ  
Query Match 2.2%; Score 12; DB 1; Length 466;  
Best Local Similarity 100.0%; Pred. No. 0.00033;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 169 FRLHCTRNVIHM 180  
Db 162 FRLHCTRNVIHM 173

```

RESULT 18
GLR_HUMAN
ID GLR_HUMAN STANDARD; PRT; 477 AA.
AC P47871;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE GLUCAGON RECEPTOR PRECURSOR (GL-R).
DE GPCR.
GN GPCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=94121651; PubMed=7507321;
RA Macneil D.J., Occi J.L., Hey P.J., Strader C.D., Graziano M.P.;
RT "Cloning and expression of a human glucagon receptor.";
RL Biochem. Biophys. Res. Commun. 198:328-334(1994).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=94192999; PubMed=8144028;
RA Lok S., Kuipjer J.L., Jelinek L.J., Kramer J.M., Whitmore T.E.,
RA Sprecher C.A., Mathewes S., Grant F.J., Biggs S.H., Rosenberg G.B.;
RT "The human glucagon receptor encoding gene: structure, cDNA sequence
RT and chromosomal localization.";
RL Gene 140:203-209(1994).
[3]
RN VARIANT SER-40.
RP MEDLINE=96034210; PubMed=7589886;
RA Fujisawa T., Ikegami H., Yamato E., Takekawa K., Nakagawa Y.,
RA Hamada Y., Ueda H., Fukuda M., Ogiwara T.;
RT "A mutation in the glucagon receptor gene (Gly40Ser): heterogeneity
RT in the association with diabetes mellitus.";
RL Diabetologia 38:983-985(1995).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON WHICH PLAYS A CENTRAL
CC ROLE IN REGULATING THE LEVEL OF BLOOD GLUCOSE BY CONTROLLING THE
CC RATE OF HEPATIC GLUCOSE PRODUCTION AND INSULIN SECRETION. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYL CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- DISEASE: IT IS A CANDIDATE FOR CERTAIN DEFECTS IN NON-INSULIN-
CC DEPENDENT DIABETES MELLITUS (NIDDM). THE VARIANT IN POSITION 40
CC (SER) IS FOUND IN SOME NIDDM PATIENTS, BUT ALSO IN NONDIABETIC
CC SUBJECTS.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL; U03469; AAC52063.1; -
DR EMBL; L20316; AAA53628.1; -
DR GCRDB; GCR_0772; -
DR GCRDB; GCR_0881; -
DR MIN; 138033; -
DR InterPro; IPR000832; -
DR Pfam; PF00002; 7tm.2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS05022; G_PROTEIN_RECEP_F2_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Polymorphism; Diabetes.
FT SIGNAL 1 25
POTENTIAL.
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FT CHAIN 26 477
FT DOMAIN 26 142
FT TRANSMEM 143 166
FT DOMAIN 167 173
FT TRANSMEM 174 193
FT DOMAIN 194 225
FT TRANSMEM 226 249
FT DOMAIN 250 263
FT TRANSMEM 264 285
FT DOMAIN 286 303
FT TRANSMEM 304 326
FT DOMAIN 327 350
FT TRANSMEM 351 369
FT DOMAIN 370 381
FT TRANSMEM 382 404
FT DOMAIN 405 477
FT CARBOHYD 46 46
FT CARBOHYD 59 59
FT CARBOHYD 74 74
FT CARBOHYD 78 78
FT VARIANT 40 40
FT SEQUENCE 477 AA; 54009 MW; ADBB477C6267AE6E CRC64;
SQ
Query Match 1.8%; Score 10; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 255 LVEGLYHLNL 264
Db 243 LVEGLYHLNL 252
RESULT 19
GLP2_RAT
ID GLP2_RAT STANDARD; PRT; 550 AA.
AC Q920W0;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GLUCAGON-LIKE PEPTIDE 2 RECEPTOR PRECURSOR (GLP-2 RECEPTOR) (GLP-2-R)
DE (GLP-2R).
GN GLP2R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Hypothalamus;
RX MEDLINE=99145591; PubMed=9990065;
RA Munroe D.G., Gupta A.K., Kooshesh F., Vyas T.B., Rizkalla G., Wang H.,
RA Demchynshyn L., Yang Z.-H., Kamboj R.K., Chen H., McCallum K.,
RA Summer-Smith M., Drucker D.J., Crivici A.;
RT "Prototypic G protein-coupled receptor for the intestinotrophic factor
RT glucagon-like peptide 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:1569-1574(1999).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON-LIKE PEPTIDE 2. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ACTIVATE ADENYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
-----
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-----
DR EMBL; AF105368; AADI6896.1; -

```









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OM protein - protein search, using sw model

Run on: September 21, 2001, 17:10:17 ; Search time 27.75 Seconds  
(without alignments)  
2579.352 Million cell updates/sec

Title: US-09-236-468A-2  
Perfect score: 541  
Sequence: 1 MAWLGLASLHWGMLGSL.....DDILMEKPSRPMESNPDTEG 541

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 425026 seqs, 132305027 residues  
Word size : 10

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SPTREMBL\_16:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mhbc:\*
- 7: sp\_mhbc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_unclassified:\*
- 13: sp\_vertebrate:\*
- 14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	7.0	169	11 Q9R1D4	Q9r1d4 mus musculus
2	27	5.0	173	13 Q9PWB7	Q9pwb7 brachydanio
3	20	3.7	94	13 Q9PRG1	Q9prg1 ictalurus p
4	18	3.3	536	13 Q9PVD3	Q9pvd3 brachydanio
5	18	3.3	595	6 Q9TU31	Q9tu31 canis.famil
6	13	2.4	418	13 Q9IBG2	Q9ibg2 gallus gall
7	13	2.4	444	13 Q9YHC6	Q9yhc6 rana ridibu
8	13	2.4	459	11 Q9JIT8	Q9jit8 mus musculus
9	13	2.4	459	11 Q9JIT40	Q9jit40 mus musculus
10	11	2.0	542	13 Q9PVD2	Q9pvd2 brachydanio
11	10	1.8	48	11 Q9JIT4	Q9jit4 mus musculus
12	10	1.8	167	13 Q9YHC8	Q9yhc8 rana ridibu

ALIGNMENTS

RESULT 1  
Q9R1D4

ID Q9R1D4 PRELIMINARY; PRT; 169 AA.  
AC Q9R1D4;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
DE PARATHYROID HORMONE TYPE-2 RECEPTOR PRECURSOR (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE=99367425; PubMed=10438471;  
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;  
RT "A G protein-coupled receptor from zebrafish is activated by human  
parathyroid hormone and not by human or teleost parathyroid hormone-  
related peptide. Implications for the evolutionary conservation of  
calcium-regulating peptide hormones.";  
RL J. Biol. Chem. 274:23035-23042(1999).  
DR EMBL; AF132083; AAD51909.1; -  
DR InterPro; IPR000832; -  
DR Pfam; PF00002; 7tm\_2; 1.  
DR PRINTS; PR00249; GPCRSECRETIN.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 169 169  
SQ SEQUENCE 169 AA; 19674 MW; 748CC8231FC69EA CRC64;

Query Match 7.0%; Score 38; DB 11; Length 169;  
Best Local Similarity 100.0%; Pred. No. 1.9e-30;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 WIYQAPILAAIGLNFILNTVRLATKIWTNAVGH 353  
DB 66 WIYQAPILAAIGLNFILNTVRLATKIWTNAVGH 103

RESULT 2

Q9PWB7  
ID Q9PWB7 PRELIMINARY; PRT; 575 AA.  
AC Q9PWB7;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE PARATHYROID HORMONE TYPE-2 RECEPTOR PRECURSOR.  
OS Brachydanio rerio (zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=KIDNEY;  
RX MEDLINE=99367425; PubMed=10438471;  
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;  
RT "A G protein-coupled receptor from zebrafish is activated by human  
parathyroid hormone and not by human or teleost parathyroid hormone-  
related peptide. Implications for the evolutionary conservation of  
calcium-regulating peptide hormones.";  
RL J. Biol. Chem. 274:23035-23042(1999).  
DR EMBL; AF132082; AAD51908.1; -  
DR InterPro; IPR000832; -  
DR InterPro; IPR001879; -  
DR Pfam; PF00002; 7tm\_2; 1.  
DR PRINTS; PR00249; GPCRSECRETIN.  
DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
DR SMART; SM00008; HormR; 1.  
KW Receptor.  
SQ SEQUENCE 575 AA; 64244 MW; 888F1C4DDB3A14DC CRC64;

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Query Match          5.0%; Score 27; DB 13; Length 575;
Best Local Similarity 100.0%; Pred. No. 9.8e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 IIGYFRLHCTRNYYIHMHFVSPMLRA 191
      |||||
Db 193 IIGYFRLHCTRNYYIHMHFVSPMLRA 219

RESULT 3
Q9PRG1 ID Q9PRG1 PRELIMINARY; PRT; 94 AA.
AC Q9PRG1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PARATHYROID HORMONE TYPE-2 RECEPTOR PRECURSOR (FRAGMENT).
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Siluriformes; Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY, AND LIVER;
RX MEDLINE=99367425; PubMed=10438471;
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
RT "A G protein-coupled receptor from zebrafish is activated by human
parathyroid hormone and not by human or teleost parathyroid hormone-
related peptide. Implications for the evolutionary conservation of
calcium-regulating peptide hormones.";
RT J. Biol. Chem. 274:23035-23042(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF132081; AAD51907.1; -.
DR EMBL; AF132078; AAD51906.1; -.
DR EMBL; AF132079; AAD51906.1; JOINED.
DR EMBL; AF132080; AAD51906.1; JOINED.
DR InterPro; IPR000832; -.
DR PRINTS; PR00249; GPCRSECRETIN.
DR ProDom; PD000303; -.
KW Receptor.
FT NON_TER 1 94
FT SEQUENCE 94 AA; 10729 MW; D949182E1D2613EF CRC64;

Query Match          3.7%; Score 20; DB 13; Length 94;
Best Local Similarity 100.0%; Pred. No. 2.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 FIVLATNYYWILVEGLYLH 262
      |||||
Db 10 FIVLATNYYWILVEGLYLH 29

RESULT 4
Q9PVD3 ID Q9PVD3 PRELIMINARY; PRT; 536 AA.
AC Q9PVD3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PARATHYROID HORMONE RECEPTOR PTH1R.
OS Brachydanio rerio (Zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99428481; PubMed=10497171;
RA Rubin D.A., Juppner H.;
RT "Zebrafish Express the Common Parathyroid Hormone/Parathyroid Hormone-
related Peptide Receptor (PTH1R) and a Novel Receptor (PTH3R) That Is
Preferentially Activated by Mammalian and Fuguish Parathyroid
Hormone-related Peptide.";
RL J. Biol. Chem. 274:28185-28190(1999).
DR EMBL; AF132084; AAF01265.1; -.
DR HSP; Q03431; IBL1.
DR InterPro; IPR000832; -.
DR InterPro; IPR001879; -.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR SMART; SM00008; Hormr; 1.
KW Receptor.
SQ SEQUENCE 536 AA; 61454 MW; 653B0A56DB2C8FA9 CRC64;

Query Match          3.3%; Score 18; DB 13; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLLHCTRNYYIHMHF 184
      |||||
Db 167 GYFRRLLHCTRNYYIHMHF 184

RESULT 5
Q9TU31 ID Q9TU31 PRELIMINARY; PRT; 595 AA.
AC Q9TU31;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PARATHYROID HORMONE RECEPTOR-1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Smock S.L., Vogt G.A., Castleberry T.A., Lu B., Owen T.A.;
RT "Molecular cloning and functional characterization of the canine
parathyroid hormone receptor-1 (PTH1).";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167095; AAD55938.1; -.
DR HSP; Q03431; IBL1.
DR InterPro; IPR000832; -.
DR InterPro; IPR001879; -.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR SMART; SM00008; Hormr; 1.
KW Receptor.
SQ SEQUENCE 595 AA; 66308 MW; 09568ECF38D4D258 CRC64;

Query Match          3.3%; Score 18; DB 6; Length 595;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYYWILVEGLYLH 262
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Db 289 YFLATNYYWILVEGLYLH 306
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RESULT 6
Q9IBG2 ID Q9IBG2 PRELIMINARY; PRT; 418 AA.
AC Q9IBG2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-WAR-2001 (TREMBlrel. 16, Last annotation update)
DE VASOACTIVE INTESTINAL PEPTIDE RECEPTOR (FRAGMENT).
GN CVIPR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Kansaku N., Shimada K., Saito N., Arakawa K., Suzuki T., Matsuda Y.,
RA Zadvorny D.;
RT "Molecular cloning of chicken VIP receptor cDNA, tissue distribution
RT and chromosomal localization.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB029895; BAA95164.1;
DR InterPro; IPR000832;
DR InterPro; IPR001879;
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR SMART; SM00008; HormR; 1.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 418 AA; 48191 MW; 7AB4796ADC808FF3 CRC64;

Query Match 2.4%; Score 13; DB 13; Length 418;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHMLF 184
DB 130 LHCTRNYIHMLF 142
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RESULT 7
Q9YHC6 ID Q9YHC6 PRELIMINARY; PRT; 444 AA.
AC Q9YHC6;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE VASOACTIVE INTESTINAL PEPTIDE/PITUITARY ADENYLATE CYCLASE ACTIVATING
DE POLYPEPTIDE RECEPTOR.
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE FROM N.A.
RA Alexandre D., Anouar Y.;
RT "A cloned frog VIP/PACAP receptor exhibits pharmacological and tissue
RT distribution characteristics of both VPAC1 and VPAC2 receptors in
RT mammals.";
RL Endocrinology 0:0-0(1999).
DR EMBL; AF100644; AAD03602.1;
DR InterPro; IPR000832;
DR InterPro; IPR001879;
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR SMART; SM00008; HormR; 1.
KW Receptor.
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SQ SEQUENCE 444 AA; 50955 MW; 883B25B729314C4C CRC64;

Query Match 2.4%; Score 13; DB 13; Length 444;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHMLF 184
DB 157 LHCTRNYIHMLF 169
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RESULT 8
Q9RIT8 ID Q9RIT8 PRELIMINARY; PRT; 459 AA.
AC Q9RIT8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-WAR-2001 (TREMBlrel. 16, Last annotation update)
DE VASOACTIVE INTESTINAL POLYPEPTIDE 1 (VPAC1) RECEPTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=129SVJ;
RX MEDLINE=99265976; PubMed=10331949;
RA Hashimoto H., Nishino A., Shintani N., Hagihara N., Copeland N.G.,
RA Jenkins N.A., Yamamoto K., Matsuda T., Ishihara T., Nagata S.,
RA Baba A.;
RT "Genomic organization and chromosomal location of the mouse vasoactive
RT intestinal polypeptide 1 (VPAC1) receptor.";
RL Genomics 58:90-93(1999).
DR EMBL; AB022860; BAA81896.1;
DR EMBL; AB022848; BAA81896.1; JOINED.
DR EMBL; AB022849; BAA81896.1; JOINED.
DR EMBL; AB022850; BAA81896.1; JOINED.
DR EMBL; AB022851; BAA81896.1; JOINED.
DR EMBL; AB022852; BAA81896.1; JOINED.
DR EMBL; AB022853; BAA81896.1; JOINED.
DR EMBL; AB022854; BAA81896.1; JOINED.
DR EMBL; AB022855; BAA81896.1; JOINED.
DR EMBL; AB022856; BAA81896.1; JOINED.
DR EMBL; AB022857; BAA81896.1; JOINED.
DR EMBL; AB022858; BAA81896.1; JOINED.
DR EMBL; AB022859; BAA81896.1; JOINED.
DR InterPro; IPR000832;
DR InterPro; IPR001879;
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR SMART; SM00008; HormR; 1.
KW Receptor.
SQ SEQUENCE 459 AA; 52094 MW; C0C3A9AE1ADF611D CRC64;

Query Match 2.4%; Score 13; DB 13; Length 459;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHMLF 184
DB 171 LHCTRNYIHMLF 183
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RESULT 9
Q9J140 ID Q9J140 PRELIMINARY; PRT; 459 AA.
AC Q9J140;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
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DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE VASOACTIVE INTESTINAL PEPTIDE RECEPTOR TYPE 1.  
GN VIPR1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N;  
RA Karacay B., O'Dorisio M.S., Kasow K., Krahe R.;  
RT "Cloning and Fine Mapping of the Vasoactive Intestinal Peptide  
Receptor I (VPAC1): A Comparative Analysis of Human, Rat and Murine  
genes.";  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF266282; AAF77053.1; -.  
DR InterPro: IPR000832; -.  
DR Pfam: PF00002; 7tm\_2; 1.  
DR PRINTS; PR00249; GPCRSECRETIN.  
DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
DR SMART; SM00008; Hormr; 1.  
KW Receptor.  
SQ SEQUENCE 459 AA; 52095 MW; 9D1ADF8567D4D7F CRC64;  
  
Query Match 2.4%; Score 13; DB 11; Length 459;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 172 LHCTRNVIHMLF 184  
Db 171 LHCTRNVIHMLF 183  
  
RESULT 10  
Q9PVD2 ID Q9PVD2 PRELIMINARY; PRT; 542 AA.  
AC Q9PVD2;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE PARATHYROID HORMONE-RELATED PROTEIN RECEPTOR PTH3R.  
OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE-99428481; PubMed=10497171;  
RA Rubin D.A., Jueppner H.;  
RT "Zebrafish Express the Common Parathyroid Hormone/Parathyroid Hormone-  
related Peptide Receptor (PTH1R) and a Novel Receptor (PTH3R) That Is  
Preferentially Activated by Mammalian and Fugu Fish Parathyroid  
Hormone-related Peptide.";  
RL J. Biol. Chem. 274:28185-28190(1999).  
DR EMBL: AF132085; AAF01266.2; -.  
DR InterPro: IPR000832; -.  
DR InterPro: IPR001879; -.  
DR Pfam: PF00002; 7tm\_2; 1.  
DR PRINTS; PR00249; GPCRSECRETIN.  
DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
DR SMART; SM00008; Hormr; 1.  
KW Receptor.  
SQ SEQUENCE 542 AA; 61438 MW; 08688658E2727303 CRC64;  
  
Query Match 2.0%; Score 11; DB 13; Length 542;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 YWILVEGLYLH 262  
Db 236 YWILVEGLYLH 246  
  
RESULT 11  
Q9JIY4 ID Q9JIY4 PRELIMINARY; PRT; 48 AA.  
AC Q9JIY4;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE GLUCAGON-LIKE PEPTIDE 2 RECEPTOR PRECURSOR (FRAGMENT).  
GN GLP2R.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SWR/J; TISSUE=SMALL INTESTINE;  
RA Bjerknes M., Cheng H.;  
RT "Clonal analysis of the effects of glucagon-like peptide 2 (GLP-2) and  
keratinocyte growth factor (KGF) on mouse intestinal epithelial  
RT progenitors.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF166265; AAF89584.1; -.  
DR InterPro: IPR000832; -.  
KW Receptor.  
FT NON\_TER 1  
FT NON\_TER 48  
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SQ SEQUENCE 48 AA; 5811 MW; 5D5B18AAEE3AF4AF CRC64;  
  
Query Match 1.8%; Score 10; DB 11; Length 48;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 172 LHCTRNVIHML 181  
Db 8 LHCTRNVIHML 17  
  
RESULT 12  
Q9VHC8 ID Q9VHC8 PRELIMINARY; PRT; 167 AA.  
AC Q9VHC8;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE GLUCAGON RECEPTOR (FRAGMENT).  
OS Rana ridibunda (Laughing frog) (Marsh frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
OX NCBI\_TaxID=8406;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PIUTITARY;  
RA Alexandre D., Anouar Y.;  
RT "A cloned frog VIP/PACAP receptor exhibits pharmacological and tissue  
RT distribution characteristics of both VPAC1 and VPAC2 receptors in  
RT mammals.";  
RL Endocrinology 0:0-0(1999).  
DR EMBL: AF100642; AAD03600.1; -.  
DR InterPro: IPR000832; -.  
DR Pfam: PF00002; 7tm\_2; 1.  
DR PRINTS; PR00249; GPCRSECRETIN.  
DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
KW Receptor.  
FT NON\_TER 1  
FT NON\_TER 167  
FT NON\_TER 167  
SQ SEQUENCE 167 AA; 19505 MW; 07AF68131034F517 CRC64;

Query Match 1.8%; Score 10; DB 13; Length 167;  
Best Local Similarity 100.0%; Pred. No. 0.081;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264  
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Db 3 LVEGLYLHNL 12

Search completed: September 21, 2001, 17:13:34  
Job time: 197 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 21, 2001, 17:08:12 ; Search time 14.41 Seconds  
(without alignments)  
773.031 Million cell updates

Title: US-09-236-468A-2  
 Perfect score: 541  
 Sequence: 1 MAWLGAASHVVGWGLMGSL.....DDILMEKPSRRPMESNPDTEG 541

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 197339 seqs, 20590346 residues

Word size : 10

Total number of hits satisfying chosen parameters: 37

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Listing first 1000 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query #			DB	ID	Description
	Score	Match	Length			
1	541	100.0	541	3	US-08-468-011A-2	Sequence 2, Appli
2	541	100.0	541	5	PCT-US95-07085-2	Sequence 2, Appli
3	60	11.1	60	3	US-08-468-011A-9	Sequence 9, Appli
4	60	11.1	60	3	US-08-468-011A-11	Sequence 11, Appli
5	60	11.1	60	3	US-08-468-011A-15	Sequence 15, Appli
6	60	11.1	60	3	US-08-468-011A-19	Sequence 19, Appli
7	59	10.9	59	3	US-08-468-011A-23	Sequence 23, Appli
8	37	6.8	37	3	US-08-468-011A-25	Sequence 25, Appli
9	37	6.8	50	3	US-08-468-011A-13	Sequence 13, Appli
10	25	4.6	60	3	US-08-468-011A-20	Sequence 20, Appli
11	25	4.6	515	2	US-08-468-249A-6	Sequence 18, Appli
12	25	4.6	585	2	US-08-468-249A-18	Sequence 6, Appli
13	25	4.6	585	1	US-08-142-439A-6	Sequence 125, App
14	25	4.6	585	2	US-08-142-551B-125	Sequence 6, Appli
15	25	4.6	585	2	US-08-869-477-6	Sequence 6, Appli
16	21	3.9	21	3	US-08-468-249A-19	Sequence 19, Appli
17	21	3.9	21	3	US-08-468-011A-21	Sequence 21, Appli
18	19	3.5	449	1	US-08-142-439A-5	Sequence 5, Appli
19	19	3.5	449	2	US-08-869-477-5	Sequence 5, Appli
20	18	3.3	591	2	US-08-468-249A-20	Sequence 20, Appli
21	14	2.6	19	2	US-08-468-249A-21	Sequence 21, Appli
22	14	2.6	19	2	US-07-864-475A-7	Sequence 7, Appli
23	14	2.6	60	3	US-08-468-249A-7	Sequence 7, Appli
24	13	2.4	458	1	US-08-468-011A-10	Sequence 10, Appli
25	13	2.4	1324	2	US-08-112-837C-2	Sequence 2, Appli
26	10	1.8	10	3	US-08-811-897A-56	Sequence 56, Appli
27	10	1.8	162	1	US-08-468-011A-17	Sequence 17, Appli
28	10	1.8	162	1	US-08-453-956-18	Sequence 18, Appli

28	10	1.8	162	1	US-08-086-631-18	Sequence 18, Appl
29	10	1.8	162	2	US-08-452-930-18	Sequence 18, Appl
30	10	1.8	162	5	PCT-US93-08174-18	Sequence 18, Appl
31	10	1.8	222	3	US-08-845-546-10	Sequence 10, Appl
32	10	1.8	477	1	US-08-453-556-25	Sequence 25, Appl
33	10	1.8	477	1	US-08-086-631-25	Sequence 25, Appl
34	10	1.8	477	2	US-08-452-930-25	Sequence 25, Appl
35	10	1.8	477	5	PCT-US93-08174-25	Sequence 25, Appl
36	10	1.8	509	3	US-08-845-546-2	Sequence 2, Appl
37	10	1.8	553	3	US-08-845-546-12	Sequence 12, Appl

## ALIGNMENTS

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		Query Match	100.0%;	Score 541;	DB 3;	Length 541;
		Best Local Similarity	100.0%;	Pred. No. 0;		
		Matches 541;	Conservative	0; Mismatches	0; Indels	0; Gaps
Qy	1	MAWLGASLHWGVMMLGSCLLARAQQLSDGTITTEEQIVLVLKAKVQCELNITAOQEGE	60			
Db	1	MAWLGASLHWGVMMLGSCLLARAQQLSDGTITTEEQIVLVLKAKVQCELNITAOQEGE	60			
Qy	61	GNCFPPEWDGLICPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDSPHSLUNKTWA	120			
Db	61	GNCFPPEWDGLICPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDSPHSLUNKTWA	120			
Qy	121	NYSDCLRFLOPDISIGKOEFCERLYVMVTWGYSTFSFGSLAVALIIIGFYRFLHCTRNVIH	180			

Db 121 NYSDCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRHCHCTRNYYH 180  
QY 181 MHLFVSFMLRATSIFFVKDRVVHAHIGVKELESIMODDPQNSIEATSVDKSQYIGCKIAV 240  
Db 181 MHLFVSFMLRATSIFFVKDRVVHAHIGVKELESIMODDPQNSIEATSVDKSQYIGCKIAV 240  
QY 241 VMFIYFLATNYWILVEGLYHNLIFVAFPSDTKYLWGFILIGWGPAAFAVAWAVARAT 300  
Db 241 VMFIYFLATNYWILVEGLYHNLIFVAFPSDTKYLWGFILIGWGPAAFAVAWAVARAT 300  
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTTRKQYRK 360  
Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTTRKQYRK 360  
QY 361 LAKSTLVLVLFVGVHYIVFVCLPHSFTGLGWEIRHMCLEFFNSFGFFVSIYCYCNGEV 420  
Db 361 LAKSTLVLVLFVGVHYIVFVCLPHSFTGLGWEIRHMCLEFFNSFGFFVSIYCYCNGEV 420  
QY 421 QAEVKKMSRWNLSDVKMRTPPCGSRRCGSVLTTVTHSTSSQSOVAAAHAWCLSLAKLPR 480  
Db 421 QAEVKKMSRWNLSDVKMRTPPCGSRRCGSVLTTVTHSTSSQSOVAAAHAWCLSLAKLPR 480  
QY 541 G 541  
Db 541 G 541

RESULT 2

PCT-US95-07085-2  
; Sequence 2, Application PC/TUS9507085  
; GENERAL INFORMATION:  
; APPLICANT: Soppet, Daniel R  
; APPLICANT: Yi, Li  
; APPLICANT: Rosen, Craig A  
; APPLICANT: Ruben, Steven  
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor  
; TITLE OF INVENTION: HLTDG74  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07068-1739  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/07085  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-393  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 541 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

PCT-US95-07085-2  
Query Match 100.0%; Score 541; DB 5; Length 541;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAWLGLASLHVWGMLGSCLLARAQLDSGTITIEEQIVLVLKAKVQCELNITAQLQEGE 60  
Db 1 MAWLGLASLHVWGMLGSCLLARAQLDSGTITIEEQIVLVLKAKVQCELNITAQLQEGE 60  
QY 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120  
Db 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120  
QY 121 NYSDCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRHCHCTRNYYH 180  
Db 121 NYSDCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRHCHCTRNYYH 180  
QY 181 MHLFVSFMLRATSIFFVKDRVVHAHIGVKELESIMODDPQNSIEATSVDKSQYIGCKIAV 240  
Db 181 MHLFVSFMLRATSIFFVKDRVVHAHIGVKELESIMODDPQNSIEATSVDKSQYIGCKIAV 240  
QY 241 VMFIYFLATNYWILVEGLYHNLIFVAFPSDTKYLWGFILIGWGPAAFAVAWAVARAT 300  
Db 241 VMFIYFLATNYWILVEGLYHNLIFVAFPSDTKYLWGFILIGWGPAAFAVAWAVARAT 300  
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTTRKQYRK 360  
Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTTRKQYRK 360  
QY 361 LAKSTLVLVLFVGVHYIVFVCLPHSFTGLGWEIRHMCLEFFNSFGFFVSIYCYCNGEV 420  
Db 361 LAKSTLVLVLFVGVHYIVFVCLPHSFTGLGWEIRHMCLEFFNSFGFFVSIYCYCNGEV 420  
QY 421 QAEVKKMSRWNLSDVKMRTPPCGSRRCGSVLTTVTHSTSSQSOVAAAHAWCLSLAKLPR 480  
Db 421 QAEVKKMSRWNLSDVKMRTPPCGSRRCGSVLTTVTHSTSSQSOVAAAHAWCLSLAKLPR 480  
QY 481 SPADSLTATSLYLAWSGVTSRTASHTLSTRNKEDSGRQDDILMEKPSRPMESNPDT 540  
Db 481 SPADSLTATSLYLAWSGVTSRTASHTLSTRNKEDSGRQDDILMEKPSRPMESNPDT 540  
QY 541 G 541  
Db 541 G 541

RESULT 3

US-08-468-011A-9  
; Sequence 9, Application US/08468011A  
; Patent No. 6030804  
; GENERAL INFORMATION:  
; APPLICANT: Soppet, Daniel R  
; APPLICANT: Yi, Li  
; APPLICANT: Rosen, Craig A  
; APPLICANT: Ruben, Steven  
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor  
; TITLE OF INVENTION: HLTDG74  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,  
; ADDRESSEE: Stewart & Olstein  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07068-1739  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1



;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/468.011A  
;; FILING DATE: 06-JUN-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MULLINS, J.G.  
;; REGISTRATION NUMBER: 33,073  
;; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201-994-1700  
;; TELEFAX: 201-994-1744  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 60 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-468-011A-9

Query Match 11.1%; Score 60; DB 3; Length 60;  
Best Local Similarity 100.0%; Pred. No. 2.6e-49;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 214 IMQDDPQNSIEATSDVKSYGCKIAVVMFYFLATNYWILVEGLYLNLIFFVAFFSDT 273  
Db 1 IMQDDPQNSIEATSDVKSYGCKIAVVMFYFLATNYWILVEGLYLNLIFFVAFFSDT 60

RESULT 4  
US-08-468-011A-11  
; Sequence 11, Application US/08468011A  
; Patent No. 6030804  
; GENERAL INFORMATION:  
; APPLICANT: Soppet, Daniel R  
; APPLICANT: Yi, Li  
; APPLICANT: Rosen, Craig A  
; APPLICANT: Ruben, Steven  
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor  
; TITLE OF INVENTION: HLTGD74  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,  
; ADDRESSEE: Stewart & Olstein  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07068-1739  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468.011A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 60 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-468-011A-11

Query Match 11.1%; Score 60; DB 3; Length 60;  
Best Local Similarity 100.0%; Pred. No. 2.6e-49;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 274 KYLMGFILIGWGFPAAFVAWAVARATLADARCWELSGADIKWIYQAPILAAIGLNFIILF 333  
Db 1 KYLMGFILIGWGFPAAFVAWAVARATLADARCWELSGADIKWIYQAPILAAIGLNFIILF 60

RESULT 5  
US-08-468-011A-15  
; Sequence 15, Application US/08468011A  
; Patent No. 6030804  
; GENERAL INFORMATION:  
; APPLICANT: Soppet, Daniel R  
; APPLICANT: Yi, Li  
; APPLICANT: Rosen, Craig A  
; APPLICANT: Ruben, Steven  
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor  
; TITLE OF INVENTION: HLTGD74  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,  
; ADDRESSEE: Stewart & Olstein  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07068-1739  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468.011A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 60 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-468-011A-15

Query Match 11.1%; Score 60; DB 3; Length 60;  
Best Local Similarity 100.0%; Pred. No. 2.6e-49;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCHNPNCTWDFMHSLNKTW 119  
Db 1 EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCHNPNCTWDFMHSLNKTW 60

RESULT 6  
US-08-468-011A-19  
; Sequence 19, Application US/08468011A  
; Patent No. 6030804  
; GENERAL INFORMATION:  
; APPLICANT: Soppet, Daniel R  
; APPLICANT: Yi, Li  
; APPLICANT: Rosen, Craig A  
; APPLICANT: Ruben, Steven

;; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor  
;; TITLE OF INVENTION: HLTG74  
;; NUMBER OF SEQUENCES: 28  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,  
;; ADDRESSEE: Stewart & Olstein  
;; STREET: 6 Becker Farm Road  
;; CITY: Roseland  
;; STATE: NJ  
;; COUNTRY: USA  
;; ZIP: 07068-1739  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 INCH DISKETTE  
;; COMPUTER: IBM PS/2  
;; OPERATING SYSTEM: MS-DOS  
;; SOFTWARE: WORD PERFECT 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/468,011A  
;; FILING DATE: 06-JUN-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MULLINS, J.G.  
;; REGISTRATION NUMBER: 33,073  
;; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201-994-1700  
;; TELEFAX: 201-994-1744  
;; INFORMATION FOR SEQ ID NO: 19:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 60 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-468-011A-19

Query Match 11.1%; Score 60; DB 3; Length 60;  
Best Local Similarity 100.0%; Pred. No. 2.6e-49;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 137 KQFECRLVMTVGVSGISFGLAVAILIIGYFRRRLHCTRNVIHMLFVSFMLRATSIPIV 196  
Db 1 KQFECRLVMTVGVSGISFGLAVAILIIGYFRRRLHCTRNVIHMLFVSFMLRATSIPIV 60

RESULT 7  
US-08-468-011A-23  
;; Sequence 23, Application US/08468011A  
;; Patent No. 6030804  
;; GENERAL INFORMATION:  
;; APPLICANT: Soppet, Daniel R  
;; APPLICANT: Yi, Li  
;; APPLICANT: Rosen, Craig A  
;; APPLICANT: Ruben, Steven  
;; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor  
;; TITLE OF INVENTION: HLTG74  
;; NUMBER OF SEQUENCES: 28  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,  
;; ADDRESSEE: Stewart & Olstein  
;; STREET: 6 Becker Farm Road  
;; CITY: Roseland  
;; STATE: NJ  
;; COUNTRY: USA  
;; ZIP: 07068-1739  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 INCH DISKETTE  
;; COMPUTER: IBM PS/2  
;; OPERATING SYSTEM: MS-DOS  
;; SOFTWARE: WORD PERFECT 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/468,011A  
;; FILING DATE: 06-JUN-1995

;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MULLINS, J.G.  
;; REGISTRATION NUMBER: 33,073  
;; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201-994-1700  
;; TELEFAX: 201-994-1744  
;; INFORMATION FOR SEQ ID NO: 23:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 59 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-468-011A-23

Query Match 10.9%; Score 59; DB 3; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.2e-48;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 387 TGLGWEIRHMCLEFNFSGGFVSIYCYCNCEVOAEVKKMSRWNLSDMKRTPPCGS 445  
Db 1 TGLGWEIRHMCLEFNFSGGFVSIYCYCNCEVOAEVKKMSRWNLSDMKRTPPCGS 59

RESULT 8  
US-08-468-011A-25  
;; Sequence 25, Application US/08468011A  
;; Patent No. 6030804  
;; GENERAL INFORMATION:  
;; APPLICANT: Soppet, Daniel R  
;; APPLICANT: Yi, Li  
;; APPLICANT: Rosen, Craig A  
;; APPLICANT: Ruben, Steven  
;; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor  
;; TITLE OF INVENTION: HLTG74  
;; NUMBER OF SEQUENCES: 28  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,  
;; ADDRESSEE: Stewart & Olstein  
;; STREET: 6 Becker Farm Road  
;; CITY: Roseland  
;; STATE: NJ  
;; COUNTRY: USA  
;; ZIP: 07068-1739  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 INCH DISKETTE  
;; COMPUTER: IBM PS/2  
;; OPERATING SYSTEM: MS-DOS  
;; SOFTWARE: WORD PERFECT 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/468,011A  
;; FILING DATE: 06-JUN-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MULLINS, J.G.  
;; REGISTRATION NUMBER: 33,073  
;; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201-994-1700  
;; TELEFAX: 201-994-1744  
;; INFORMATION FOR SEQ ID NO: 25:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 37 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-468-011A-25

Query Match 6.8%; Score 37; DB 3; Length 37;  
Best Local Similarity 100.0%; Pred. No. 8e-28;

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RESULT 10
US-08-468-011A-20
; Sequence 20, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: H1TDG74
; NUMBER OF SEQUENCES: 28

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; ORGANISM: Didelphis virginiana
; US-08-142-439A-6

Query Match          4.6%; Score 25; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 GYFRLHCTRNYYIHMLFVSPMLRA 191
      |||
Db 207 GYFRLHCTRNYYIHMLFVSPMLRA 231

RESULT 13
US-08-142-551B-125
; Sequence 125, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142.551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..585
; OTHER INFORMATION: /note= "PTH receptor"
; US-08-142-551B-125

Query Match          4.6%; Score 25; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 GYFRLHCTRNYYIHMLFVSPMLRA 191

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DB 207 GYFRLHCTRNVIHMLFVSEMLRA 231
|||||
RESULT 14
US-08-869-477-6
; Sequence 6, Application US/08869477
; Patent No. 5846747
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5846747o No. 5846747disk of No. 5846747th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,477
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439
; FILING DATE: 24-NOV-93
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Didelphis virginiana
US-08-869-477-6

Query Match 4.6%; Score 25; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 GYFRLHCTRNVIHMLFVSEMLRA 191
|||||
Db 207 GYFRLHCTRNVIHMLFVSEMLRA 231

RESULT 15
US-08-468-249A-19
; Sequence 19, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.

Query Match 4.6%; Score 25; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 GYFRLHCTRNVIHMLFVSEMLRA 191
|||||
Db 207 GYFRLHCTRNVIHMLFVSEMLRA 231

RESULT 16
US-08-468-011A-21
; Sequence 21, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTDG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
```

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; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-21

Query Match 3.9%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 KDRVVHAHIGVKESLIMQD 217
Db 1 KDRVVHAHIGVKESLIMQD 21

RESULT 17
US-08-142-439A-5
; Sequence 5, Application US/08142439A
; Patent No. 5670360
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5670360o No. 5670360disk of No. 5670360th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439A
; FILING DATE: 24-NOV-93
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION NUMBER: PCT/EP93/00697
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus norvegicus
; STRAIN: Sprague-Dawley
; US-08-869-477-5

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus norvegicus
; STRAIN: Sprague-Dawley
; US-08-142-439A-5

Query Match 3.5%; Score 19; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 6.8e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRNHYHMLFVSF 187
Db 167 FRRLHCTRNHYHMLFVSF 185

RESULT 18
US-08-869-477-5
; Sequence 5, Application US/08869477
; Patent No. 5846747
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5846747o No. 5846747disk of No. 5846747th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,477
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439
; FILING DATE: 24-NOV-93
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus norvegicus
; STRAIN: Sprague-Dawley
; US-08-869-477-5

```

US-08-468-249A-21  
; Sequence 21, Application US/08468249A  
; Patent No. 5886148  
; GENERAL INFORMATION:  
; APPLICANT: Seure et al., Gino V.

; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/864,475A  
; FILING DATE: 04-06-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/681,702  
; FILING DATE: 05-04-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul T. Clark  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/071002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; US-07-864-475A-7

Query Match 2.6%; Score 14; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEG 258  
|||||  
DB 6 YFLATNYWILVEG 19

RESULT 22  
US-08-468-249A-7  
; Sequence 7, Application US/08468249A  
; Patent No. 5886148  
; GENERAL INFORMATION:  
; APPLICANT: Segre et al., Gino V.  
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA  
; TITLE OF INVENTION: ENCODING SAME  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,249A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/864,475  
; FILING DATE: 06-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/681,702  
; FILING DATE: 04-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 00786/071003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-468-249A-7

Query Match 2.6%; Score 14; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEG 258  
|||||  
DB 6 YFLATNYWILVEG 19

RESULT 23  
US-08-468-011A-10  
; Sequence 10, Application US/08468011A  
; Patent No. 6030804  
; GENERAL INFORMATION:  
; APPLICANT: Soppet, Daniel R  
; APPLICANT: Yi, Li  
; APPLICANT: Rosen, Craig A  
; APPLICANT: Ruben, Steven  
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor  
; TITLE OF INVENTION: HLTG74  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,  
; ADDRESSEE: Stewart & Oistein  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07068-1739  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,011A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 60 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-468-011A-10

Query Match 2.6%; Score 14; DB 3; Length 60;  
Best Local Similarity 100.0%; Pred. No. 5.9e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 TNYWILVEGLYLH 262  
|||||  
DB 36 TNYWILVEGLYLH 49



RESULT 24  
US-08-112-817C-2  
; Sequence 2, Application US/08112817C  
; Patent No. 5573928  
; GENERAL INFORMATION:  
; APPLICANT: Hsiung, Hansen M.  
; APPLICANT: Smith, Dennis P.  
; APPLICANT: Zhang, Xing-Yue  
; TITLE OF INVENTION: PORCINE VASOACTIVE INTESTINAL PEPTIDE  
; TITLE OF INVENTION: RECEPTOR  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: USA  
; ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh IIfx compatible  
; OPERATING SYSTEM: System 7  
; SOFTWARE: Microsoft Word for Macintosh v.5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/112.817C  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murphy, Richard B.  
; REGISTRATION NUMBER: 35,296  
; REFERENCE/DOCKET NUMBER: X-9293  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 317-276-3589  
; TELEFAX: 317-276-1294  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 458 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-112-817C-2

Query Match 2.4%; Score 13; DB 1; Length 458;  
Best Local Similarity 100.0%; Pred. No. 0.00031;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNVIHMLF 184  
| | | | | | | | | |  
Db 171 LHCTRNVIHMLF 183

RESULT 25  
US-08-811-897A-56  
; Sequence 56, Application US/08811897A  
; Patent No. 5858787  
; GENERAL INFORMATION:  
; APPLICANT: ONDA, Haruo  
; APPLICANT: OHTAKI, Tetsuya  
; APPLICANT: MASUDA, Yasushi  
; APPLICANT: KITADA, Chieko  
; APPLICANT: ISHIBASHI, Yoshihiro  
; APPLICANT: HOSoya, Masaki  
; APPLICANT: OGI, Kazuhiro  
; APPLICANT: MIYAMOTO, Yasunori  
; APPLICANT: HABA, Yugo  
; APPLICANT: SHIMAMOTO, No. 58587871c  
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR PREPARING  
; TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &

; ADDRESSEE: CUSHMAN  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/811.897A  
; FILING DATE: 05-MAR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/202,986  
; FILING DATE: February 25, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, David S.  
; REGISTRATION NUMBER: 34235  
; REFERENCE/DOCKET NUMBER: 44168-DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)523-3400  
; TELEFAX: (617)523-6440  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1324 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-811-897A-56

Query Match 2.4%; Score 13; DB 2; Length 1324;  
Best Local Similarity 100.0%; Pred. No. 0.00081;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNVIHMLF 184  
| | | | | | | | | |  
Db 173 LHCTRNVIHMLF 185

RESULT 26  
US-08-468-011A-17  
; Sequence 17, Application US/08468011A  
; Patent No. 6030804  
; GENERAL INFORMATION:  
; APPLICANT: Soppet, Daniel R  
; APPLICANT: Yi, Li  
; APPLICANT: Rosen, Craig A  
; APPLICANT: Ruben, Steven  
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor  
; TITLE OF INVENTION: HLTG74  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,  
; ADDRESSEE: Stewart & Oistein  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07068-1739  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468.011A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:

NAME: MULLINS, J.G.  
REGISTRATION NUMBER: 33,073  
REFERENCE/DOCKET NUMBER: 325800-458 (PF201)  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-468-011A-17

Query Match 1.8%; Score 10; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.007;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 ANYSDCLRFL 129  
DB 1 ANYSDCLRFL 10  
|||||

RESULT 27  
US-08-453-956-18  
Sequence 18, Application US/08453956  
Patent No. 5770445  
GENERAL INFORMATION:  
APPLICANT: Kindsvogel, Wayne R.  
TITLE OF INVENTION: GLUCAGON RECEPTORS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY  
STREET: 6300 COLUMBIA CENTER  
CITY: SEATTLE  
STATE: WA  
COUNTRY: USA  
ZIP: 99104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/453,956  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/086,631  
FILING DATE: July 1, 1993  
APPLICATION NUMBER: US 07/938,331  
FILING DATE: 28-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 990008.424C1  
TELEPHONE: 206-622-4900  
TELEFAX: 206-682-6031  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 162 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-453-956-18

Query Match 1.8%; Score 10; DB 1; Length 162;  
Best Local Similarity 100.0%; Pred. No. 0.084;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264  
DB 99 LVEGLYLHNL 108  
|||||

RESULT 28  
US-08-086-631-18  
Sequence 18, Application US/08086631  
Patent No. 5776725  
GENERAL INFORMATION:  
APPLICANT: Kindsvogel, Wayne R.  
TITLE OF INVENTION: GLUCAGON RECEPTORS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY  
STREET: 6300 COLUMBIA CENTER  
CITY: SEATTLE  
STATE: WA  
COUNTRY: USA  
ZIP: 99104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/086,631  
FILING DATE: July 1, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/938,331  
FILING DATE: 28-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 990008.424C1  
TELEPHONE: 206-622-4900  
TELEFAX: 206-682-6031  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 162 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-086-631-18

Query Match 1.8%; Score 10; DB 1; Length 162;  
Best Local Similarity 100.0%; Pred. No. 0.084;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264  
DB 99 LVEGLYLHNL 108  
|||||

RESULT 29  
US-08-452-930-18  
Sequence 18, Application US/08452930  
Patent No. 5919635  
GENERAL INFORMATION:  
APPLICANT: Kindsvogel, Wayne R.  
TITLE OF INVENTION: GLUCAGON RECEPTORS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY  
STREET: 6300 COLUMBIA CENTER  
CITY: SEATTLE  
STATE: WA  
COUNTRY: USA  
ZIP: 99104-7092  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/452,930  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: .435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/086,631  
FILING DATE: July 1, 1993  
APPLICATION NUMBER: US 07/938,331  
FILING DATE: 28-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 990008.424C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
TELEFAX: 206-682-6031  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 162 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-08174-18

Query Match 1.8%; Score 10; DB 2; Length 162;  
Best Local Similarity 100.0%; Pred. No. 0.084;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 LVEGLYHLNL 264  
|||||  
Db 99 LVEGLYHLNL 108

RESULT 30  
PCT-US93-08174-18  
Sequence 18, Application PC/TUS9308174  
GENERAL INFORMATION:  
APPLICANT: NAME: ZymoGenetics, Inc.  
APPLICANT: STREET: 4225 Roosevelt Way  
APPLICANT: CITY: Seattle, Washington  
APPLICANT: COUNTRY: United States  
APPLICANT: POSTAL CODE: 98105  
APPLICANT: TELEPHONE: (206) 547-80808  
TITLE OF INVENTION: GLUCAGON RECEPTORS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY  
STREET: 6300 COLUMBIA CENTER  
CITY: SEATTLE  
STATE: WA  
COUNTRY: USA  
ZIP: 99104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08174  
FILING DATE: 30-AUG-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/086,631  
FILING DATE: July 1, 1993  
APPLICATION NUMBER: US 07/938,331  
FILING DATE: 28-AUG-1992  
ATTORNEY/AGENT INFORMATION:

NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 990008.424C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
TELEFAX: 206-682-6031  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 162 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-08174-18

Query Match 1.8%; Score 10; DB 5; Length 162;  
Best Local Similarity 100.0%; Pred. No. 0.084;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 LVEGLYHLNL 264  
|||||  
Db 99 LVEGLYHLNL 108

RESULT 31  
US-08-845-546-10  
Sequence 10, Application US/08845546  
Patent No. 6077949  
GENERAL INFORMATION:  
APPLICANT: Munroe, Donald  
APPLICANT: Gupta, Ashwani  
APPLICANT: Vyas, Tejpal  
APPLICANT: McCallum, Kirk  
APPLICANT: Fan, Ermei  
TITLE OF INVENTION: CLONED GLUCAGON-LIKE PEPTIDE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/845,546  
FILING DATE: 24-APR-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Friebe, Thomas E.  
REGISTRATION NUMBER: 29,258  
REFERENCE/DOCKET NUMBER: 8607-018  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 222 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-845-546-10

Query Match 1.8%; Score 10; DB 3; Length 222;  
Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYIHM 181  
          |||||  
Db 20 LHCTRYIHM 29

## RESULT 32

US-08-453-956-25  
; Sequence 25, Application US/08453956  
; Patent No. 5770445  
; GENERAL INFORMATION:  
; APPLICANT: Kindsvogel, Wayne R.  
; TITLE OF INVENTION: GLUCAGON RECEPTORS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY  
; STREET: 6300 COLUMBIA CENTER  
; CITY: SEATTLE  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 99104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/453,956  
; FILING DATE: 30-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/086,631  
; FILING DATE: July 1, 1993  
; APPLICATION NUMBER: US 07/938,331  
; FILING DATE: 28-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 990008.424C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; TELEFAX: 206-682-6031  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 477 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-453-956-25

Query Match 1.8%; Score 10; DB 1; Length 477;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264  
          |||||  
Db 243 LVEGLYLHNL 252

## RESULT 33

US-08-086-631-25  
; Sequence 25, Application US/08086631  
; Patent No. 5776725  
; GENERAL INFORMATION:  
; APPLICANT: Kindsvogel, Wayne R.  
; TITLE OF INVENTION: GLUCAGON RECEPTORS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY  
; STREET: 6300 COLUMBIA CENTER  
; CITY: SEATTLE

; STATE: WA  
; COUNTRY: USA  
; ZIP: 99104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/086,631  
; FILING DATE: July 1, 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/938,331  
; FILING DATE: 28-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 990008.424C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; TELEFAX: 206-682-6031  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 477 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-086-631-25

Query Match 1.8%; Score 10; DB 1; Length 477;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264  
          |||||  
Db 243 LVEGLYLHNL 252

## RESULT 34

US-08-452-930-25  
; Sequence 25, Application US/08452930  
; Patent No. 5919635  
; GENERAL INFORMATION:  
; APPLICANT: Kindsvogel, Wayne R.  
; TITLE OF INVENTION: GLUCAGON RECEPTORS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY  
; STREET: 6300 COLUMBIA CENTER  
; CITY: SEATTLE  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 99104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/452,930  
; FILING DATE: 30-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/086,631  
; FILING DATE: July 1, 1993  
; APPLICATION NUMBER: US 07/938,331  
; FILING DATE: 28-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 990008.424C1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
TELEFAX: 206-682-6031  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 477 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-452-930-25

Query Match 1.8%; Score 10; DB 2; Length 477;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264  
|||||

DB 243 LVEGLYLHNL 252

## RESULT 35

PCT-US93-08174-25

Sequence 25, Application PC/TUS9308174

GENERAL INFORMATION:

APPLICANT:

APPLICANT: NAME: ZymoGenetics, Inc.

APPLICANT: STREET: 4225 Roosevelt Way North East

APPLICANT: CITY: Seattle, Washington

APPLICANT: COUNTRY: United States

APPLICANT: POSTAL CODE: 98105

APPLICANT: TELEPHONE: (206) 547-8080

TITLE OF INVENTION: GLUCAGON RECEPTORS

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED AND BERRY

STREET: 6300 COLUMBIA CENTER

CITY: SEATTLE

STATE: WA

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08174

FILING DATE: 30-AUG-1993

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/086,631

FILING DATE: July 1, 1993

APPLICATION NUMBER: US 07/938,331

FILING DATE: 28-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: McMasters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 990008.424C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900

TELEFAX: 206-682-6031

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 477 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US93-08174-25

Query Match 1.8%; Score 10; DB 5; Length 477;  
Best Local Similarity 100.0%; Pred. No. 0.22;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264

|||||

DB 243 LVEGLYLHNL 252

## RESULT 36

US-08-845-546-2

Sequence 2, Application US/08845546

Patent No. 6077949

GENERAL INFORMATION:

APPLICANT: Munroe, Donald

APPLICANT: Gupta, Ashwani

APPLICANT: Vyas, Tejal

APPLICANT: McCallum, Kirk

APPLICANT: Fan, Ermei

TITLE OF INVENTION: CLONED GLUCAGON-LIKE PEPTIDE

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie &amp; Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/845,546

FILING DATE: 24-APR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Friebe, Thomas E.

REGISTRATION NUMBER: 29,258

REFERENCE/DOCKET NUMBER: 8607-018

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 509 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-845-546-2

Query Match 1.8%; Score 10; DB 3; Length 509;

Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHM 181

|||||

DB 165 LHCTRNVIHM 174

## RESULT 37

US-08-845-546-12

Sequence 12, Application US/08845546

Patent No. 6077949

GENERAL INFORMATION:

APPLICANT: Munroe, Donald

APPLICANT: Gupta, Ashwani

APPLICANT: Vyas, Tejal

APPLICANT: McCallum, Kirk

APPLICANT: Fan, Ermei

;; TITLE OF INVENTION: CLONED GLUCAGON-LIKE PEPTIDE  
;; TITLE OF INVENTION: 2 RECEPTORS  
;; NUMBER OF SEQUENCES: 24  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Pennie & Edmonds LLP  
;; STREET: 1155 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 10036-2711  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/845,546  
;; FILING DATE: 24-APR-1997  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Friebe, Thomas E.  
;; REGISTRATION NUMBER: 29,258  
;; REFERENCE/DOCKET NUMBER: 8607-018  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 212-790-9090  
;; TELEFAX: 212-869-8864  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 12:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 553 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: protein  
US-08-845-546-12

Query Match 1.8%; Score 10; DB 3; Length 553;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNHYHM 181  
|  
Db 206 LHCTRNHYHM 215

Search completed: September 21, 2001, 17:10:15  
Job time: 123 sec